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(54) **PLANT WITH REDUCED PROTEIN PRODUCTIVITY IN SEEDS, AND METHOD FOR PRODUCING SAME**

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(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

According to the present invention, a gene having a novel function that can cause an increase or decrease in seed protein content is searched for. A chimeric protein obtained by fusing a transcription factor consisting of a protein comprising an amino acid sequence shown in any of the even-numbered SEQ ID NOS: 1 to 76 and a functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor or a transcription factor consisting of a protein comprising an amino acid sequence shown in any of the even-numbered SEQ ID NOS: 77 to 84 is expressed in a plant.

4 Claims, No Drawings

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**PLANT WITH REDUCED PROTEIN
PRODUCTIVITY IN SEEDS, AND METHOD
FOR PRODUCING SAME**

**CROSS REFERENCE TO RELATED
APPLICATIONS**

This application is a National Stage of International Application No. PCT/JP2010/059495 filed Jun. 4, 2010, claiming priority based on Japanese Patent Application No. 2009-135195, filed Jun. 4, 2009, the contents of all of which are incorporated herein by reference in their entirety.

BACKGROUND ART

In order to change the amount of protein in seeds, the following have been conventionally used: (1) an improved cultivation method; (2) a method for processing harvested seeds, and particularly grains such as rice grains, with an acid or bacterium; (3) molecular breeding using markers; (4) mutant screening; (5) gene recombination; and other methods.

Problems relating to the above methods and the object achieved by the present invention are described below.

According to the method (1) above, it is possible to change the protein amount, although it is only possible to increase or decrease the amount to a slight extent. In addition, although the method (2) above is effective to a certain extent for reducing the protein amount, processing of harvested seeds is labor- and time-consuming. Further, advantageous results such as an increase in protein amount cannot be obtained according to the method (2) above. According to the method (3) above, the protein amount is determined to be a quantitative trait. In order to modify such trait by a conventional breeding method, it is necessary to identify a plurality of gene loci that contribute highly to trait expression by QTL analysis, to specify the causative gene at each gene locus, and to introduce each causative gene into a desired variety by crossing. Therefore, the method (3) above is also labor- and time-consuming. With the method (4) above, a low-glutelin rice line such as LGC-1 is bred. However, the amount of remaining glutelin accounts for 30% to 50% of that in the original variety. In addition, there are problematic points common to low-glutelin rice lines. In fact, the amount of glutelin, which is an easily digestible protein, decreases to significantly below the level found in the original variety. However, this in turn causes a significant increase in the amount of prolamin, which is an indigestible protein. Therefore, the method (4) above cannot be evaluated as a method for reducing total seed protein content. In the case of the method (5) above, it has been reported that the total expression level of the prolamin multigene group was remarkably reduced, resulting in reduction of the protein content in rice seeds (Patent Document 1:WO2004/056993). However, in this case, the decrease in the total protein content is 15% at maximum, although the amount of prolamin itself decreases to 50% or less of the original amount. In addition, regarding the method (5) above, it has been reported that transcription factors specified by AT1G04550, AT1G66390, AT5G13330, and At2g30420 were overexpressed in *Arabidopsis thaliana* seeds, which resulted in, respectively, 25%, 14%, 39%, and 17% increases in protein content. Also, it has been reported that overexpression of a transcription factor specified by At2g47460 resulted in a decrease in the seed storage protein content of 13% (Patent Document 2: WO 01/35727).

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In spite of the development of the above molecular breeding methods for the improvement of a variety of traits, there are still no practically available techniques to increase or decrease seed protein content.

As reasons for the above, it is considered that truly excellent genes remain undiscovered, and that new recombinant varieties that have been confirmed to have desirable effects in the test phase cannot exhibit expected effects upon practical use in different environments. In addition, a number of genes are involved in the expression of quantitative traits such as seed protein content in different steps in the control system, the metabolizing system, and other systems. Thus, it has been difficult to discover or develop truly excellent genes capable of improving quantitative traits. In order to solve such problems, an object of the present invention is to find a novel gene exhibiting remarkably high effects. Another object of the present invention is to develop a gene capable of exerting effects in a practical environment to an extent comparable to the effects exerted in the test phase.

CITATION LIST

Patent Literature

- Patent Document 1: WO2004/056993
Patent Document 2: WO 01/35727

SUMMARY OF INVENTION

Technical Problem

In view of the above circumstances, an object of the present invention is to provide a technique for searching for a gene having a novel function that can cause an increase or decrease in seed protein content so as to improve such feature of a plant.

Solution to Problem

As a result of intensive studies to achieve the above objects, the present inventors found that it is possible to improve various quantitative traits and particularly to increase or decrease seed protein content via induction of expression of a chimeric protein obtained by fusing a particular transcription factor and a functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor (hereinafter sometimes referred to as a "repressor domain"), introduction of a particular gene encoding a particular transcription factor, or modification of an expression control region of an endogenous gene corresponding to the gene. This has led to the completion of the present invention.

The plant of the present invention is obtained by inducing expression of a chimeric protein in a plant, such chimeric protein obtained by fusing a transcription factor consisting of any one of the following proteins (a) to (c) and a functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor, introducing a gene encoding a transcription factor consisting of any one of the following proteins (d) to (f) into a plant, or modifying an expression control region of an endogenous gene corresponding to the gene in a plant.

- (a) A protein comprising an amino acid sequence shown in any of the even-numbered SEQ ID NOS: 1 to 76
 (b) A protein having transactivation activity and comprising an amino acid sequence that has a deletion, a substitution, an addition, or an insertion of one or a plurality of amino

- acids with respect to an amino acid sequence shown in any of the even-numbered SEQ ID NOS: 1 to 76.
- (c) A protein having transactivation activity encoded by a polynucleotide that hybridizes under stringent conditions to a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence shown in any of the odd-numbered SEQ ID NOS: 1 to 76.
- (d) A protein comprising an amino acid sequence shown in any of the even-numbered SEQ SEQ ID NOS: 77 to 84.
- (e) A protein having transactivation activity and comprising an amino acid sequence that has a deletion, a substitution, an addition, or an insertion of one or a plurality of amino acids with respect to the amino acid sequence shown in any of the even-numbered SEQ ID NOS: 77 to 84.
- (f) A protein having transactivation activity encoded by a polynucleotide that hybridizes under stringent conditions to a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence shown in any of the odd-numbered SEQ ID NOS: 77 to 84.

Preferably, the fusion of a functional peptide with a predetermined transcription factor causes repression of transcriptional regulatory activity, and particularly, transactivation activity, of the transcription factor in the plant of the present invention. Examples of the above functional peptide used herein include peptides expressed by the following formulae (1) to (8).

(1) X1-Leu-Asp-Leu-X2-Leu-X3 (SEQ ID NO: 392 with deletion of 0-10 residues from the N-terminus)

(where X1 denotes a set of 0 to 10 amino acid residues, X2 denotes Asn or Glu, and X3 denotes a set of at least 6 amino acid residues.)

(2) Y1-Phe-Asp-Leu-Asn-Y2-Y3 (SEQ ID NO: 393 with deletion of 0-10 residues from the N-terminus)

(where Y1 denotes a set of 0 to 10 amino acid residues, Y2 denotes Phe or Ile, and Y3 denotes a set of at least 6 amino acid residues.)

(3) Z1-Asp-Leu-Z2-Leu-Arg-Leu-Z3 (SEQ ID NO: 394 with deletion of 0-10 residues from the C-terminus and deletion of 0-2 residues from the N-terminus)

(where Z1 denotes Leu, Asp-Leu, or Leu-Asp-Leu, Z2 denotes Glu, Gln, or Asp, and Z3 denotes a set of 0 to 10 amino acid residues.)

(4) Asp-Leu-Z4-Leu-Arg-Leu (residues 4-9 of SEQ ID NO: 394)

(where Z4 denotes Glu, Gln, or Asp.)

(5) $\alpha 1$ -Leu- $\beta 1$ -Leu- $\gamma 1$ -Leu (SEQ ID NO: 395)

(6) $\alpha 1$ -Leu- $\beta 1$ -Leu- $\gamma 2$ -Leu (SEQ ID NO: 396)

(7) $\alpha 1$ -Leu- $\beta 2$ -Leu-Arg-Leu (SEQ ID NO: 397)

(8) $\alpha 2$ -Leu- $\beta 1$ -Leu-Arg-Leu (SEQ ID NO: 398)

(where $\alpha 1$ denotes Asp, Asn, Glu, Gln, Thr, or Ser, $\alpha 2$ denotes Asn, Glu, Gln, Thr, or Ser, $\beta 1$ denotes Asp, Gln, Asn, Arg, Glu, Thr, Ser, or His, $\beta 2$ denotes Asn, Arg, Thr, Ser, or His, $\gamma 1$ denotes Arg, Gln, Asn, Thr, Ser, His, Lys, or Asp, and $\gamma 2$ denotes Gln, Asn, Thr, Ser, His, Lys, or Asp in formulae (5) to (8).)

In addition, the plant of the present invention provides significant improvement or reduction of productivity of a protein contained in seeds. Here, the expression "significant improvement or reduction" indicates that the plant of the present invention allows an increase or decrease in the seed protein content associated with a statistically significant difference when compared in terms of material productivity with a plant in which the above chimeric protein is not expressed.

Meanwhile, according to the present invention, the above chimeric protein, the gene encoding the chimeric protein, an expression vector comprising the gene, and a transformant comprising the gene can be provided.

This description includes part or all of the contents as disclosed in the description and/or drawings of Japanese Patent Application No. 2009-135195, which is a priority document of the present application.

Advantageous Effects of Invention

The seed protein content is improved or reduced in the plant of the present invention. Therefore, the use of the plant of the present invention enables mass production of a desired protein in seeds of the plant. Alternatively, seeds that exhibit a significant reduction in the content of a protein contained as an impurity or an allergen can be produced.

DESCRIPTION OF EMBODIMENTS

The present invention will be described in detail as follows.

The plant of the present invention is a plant in which a chimeric protein obtained by fusing a predetermined transcription factor and a functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor is expressed, a plant in which a gene encoding a predetermined transcription factor is present as a result of gene introduction, or a plant in which an expression control region of an endogenous gene corresponding to the gene is modified. The plant of the present invention is found to exhibit significant improvement or reduction of the productivity of seed protein when compared with a wild-type plant. Specifically, the plant of the present invention is produced by causing a transcription factor to be expressed in the form of a chimeric protein with the functional peptide in a desired plant, introducing a gene encoding a predetermined transcription factor into a desired plant, or modifying an expression control region of an endogenous gene corresponding to the gene in a desired plant so as to significantly improve or reduce the protein content in seeds of the desired plant. Here, the expression level of the gene can be significantly increased compared with that in a wild-type plant by exogenously introducing a predetermined transcription factor into a plant or modifying an expression control region of an endogenous gene corresponding to the gene in a plant. The plant according to the present invention may be produced by causing the expression of the predetermined transcription factor in all plant tissues, or at least in some plant tissues. Here, the term "plant tissue(s)" is meant to include plant organ(s) such as leaves, stems, seeds, roots, and flowers.

Also, the term "expression control region" refers to a promoter region to which RNA polymerase binds and a region to which another transcription factor binds. A transcriptional regulatory region is preferably modified by substituting a promoter region, for example, among endogenous transcriptional regulatory regions with a promoter region that enables a higher expression level. In addition, when replacing, for example, a promoter region with a promoter region that enables a higher expression level, it becomes possible to cause overexpression of the predetermined transcription factor. Further, the term "overexpression" used herein also indicates a case in which a gene encoding a predetermined transcription factor present in a plant as a result of gene introduction is transcribed and thus is expressed at a level at which the gene can be confirmed as a transcription product.

In particular, preferably, the transactivation activity of a transcription factor is repressed in the plant of the present invention by fusing the factor with the above functional peptide. In other words, when a chimeric protein obtained by fusing a transcription factor with the functional peptide is expressed in the plant of the present invention, this preferably

results in expression of transcription repression effects originally imparted to the functional peptide as a dominant trait.

A protein contained in a plant used herein may be any protein originally accumulated in seeds and any protein encoded by a gene exogenously introduced into the plant. In addition, genes to be exogenously introduced are introduced under control of, for example, a publicly known seed-specific expression promoter, thereby allowing efficient expression of the genes in seeds.

In particular, if the seed protein content increases, purification cost or transport cost can be reduced. Thus, such plant is highly industrially applicable. Meanwhile, a protein contained in seeds might become an impurity or allergen, depending on the usage of seeds. Therefore, if the productivity of a protein contained in seeds decreases, the impurity content or the allergen content also decreases. In such case, the seeds are highly industrially applicable.

Plants used herein are not particularly limited, and thus any plant can be used as a target plant. Examples of an available target plant include soybean, sesame, olive oil, coconut, rice, cotton, sunflower, corn, sugarcane, *Jatropha*, palm, tobacco, safflower, and rapeseed. Also, *Arabidopsis thaliana*, which has been widely used as an biological model for plant gene analysis and for which gene expression analysis methods have been established, can be used as a target plant.

In addition, transcription repression activity of a chimeric protein comprising a transcription factor is activity of recognizing a cis sequence that is recognized by the transcription factor or a cis sequence of a different transcription factor that is analogous to such a cis sequence so as to actively repress the expression of downstream genes. Thus, such chimeric protein can also be called a "transcriptional repressor." A method for causing a chimeric protein comprising a transcription factor to have transcription repression activity is not particularly limited. However, the most preferable method may be a method for constructing a chimeric protein (fusion protein) by adding a repressor domain sequence or an SRDX sequence thereto.

In the above method, as a repressor domain sequence, a variety of amino acid sequences discovered by the present inventors, each of which constitutes a peptide capable of converting an arbitrary transcription factor into a transcriptional repressor, can be used. For example, the following can be referred to for a method using a repressor domain sequence: JP Patent Publication (Kokai) No. 2001-269177A; JP Patent Publication (Kokai) No. 2001-269178A; JP Patent Publication (Kokai) No. 2001-292776A; JP Patent Publication (Kokai) No. 2001-292777A; JP Patent Publication (Kokai) No. 2001-269176A; JP Patent Publication (Kokai) No. 2001-269179A; WO03/055903; Ohta, M., Matsui, K., Hiratsu, K., Shinshi, H. and Ohme-Takagi, M., The Plant Cell, Vol. 13, 1959-1968, August, 2001; and Hiratsu, K., Ohta, M., Matsui, K., or Ohme-Takagi, M., FEBS Letters 514(2002) 351-354. A repressor domain sequence can be excised from a Class II ERF (Ethylene Responsive Element Binding Factor) protein or a plant zinc finger protein (zinc finger protein such as *Arabidopsis thaliana* SUPERMAN protein). The sequence has a very simple structure.

Examples of a transcription factor constituting a chimeric protein to be expressed include transcription factors specified by AGI codes for *Arabidopsis thaliana* listed in tables 1 and 2. In addition, any transcription factor listed in table 1 causes a significant increase in seed protein content when a chimeric protein comprising the transcription factor and a repressor domain is expressed in a plant. Meanwhile, any transcription factor listed in table 2 causes a significant decrease in seed

protein content when a chimeric protein comprising the transcription factor and a repressor domain is expressed in a plant.

TABLE 1

AGI code	Nucleotide sequence	Amino acid sequence
AT2G23760	SEQ ID NO: 1	SEQ ID NO: 2
AT1G18330	SEQ ID NO: 3	SEQ ID NO: 4
AT2G02070	SEQ ID NO: 5	SEQ ID NO: 6
AT1G12980	SEQ ID NO: 7	SEQ ID NO: 8
AT5G62380	SEQ ID NO: 9	SEQ ID NO: 10
AT4G23750	SEQ ID NO: 11	SEQ ID NO: 12
AT4G32800	SEQ ID NO: 13	SEQ ID NO: 14
AT1G24590	SEQ ID NO: 15	SEQ ID NO: 16
AT5G07690	SEQ ID NO: 17	SEQ ID NO: 18
AT1G71692	SEQ ID NO: 19	SEQ ID NO: 20
AT1G52150	SEQ ID NO: 21	SEQ ID NO: 22
AT3G25890	SEQ ID NO: 23	SEQ ID NO: 24
AT1G09540	SEQ ID NO: 25	SEQ ID NO: 26
AT5G22380	SEQ ID NO: 27	SEQ ID NO: 28
AT2G44940	SEQ ID NO: 29	SEQ ID NO: 30
AT5G41030	SEQ ID NO: 31	SEQ ID NO: 32
AT5G60970	SEQ ID NO: 33	SEQ ID NO: 34
AT5G35550	SEQ ID NO: 35	SEQ ID NO: 36
AT1G60240	SEQ ID NO: 37	SEQ ID NO: 38
AT2G23290	SEQ ID NO: 39	SEQ ID NO: 40
AT5G14000	SEQ ID NO: 41	SEQ ID NO: 42
AT1G19490	SEQ ID NO: 43	SEQ ID NO: 44

TABLE 2

AGI code	Nucleotide sequence	Amino acid sequence
AT1G32770	SEQ ID NO: 45	SEQ ID NO: 46
AT5G47220	SEQ ID NO: 47	SEQ ID NO: 48
AT1G56650	SEQ ID NO: 49	SEQ ID NO: 50
AT1G63910	SEQ ID NO: 51	SEQ ID NO: 52
AT3G15510	SEQ ID NO: 53	SEQ ID NO: 54
AT2G45680	SEQ ID NO: 55	SEQ ID NO: 56
AT2G31230	SEQ ID NO: 57	SEQ ID NO: 58
AT1G12260	SEQ ID NO: 59	SEQ ID NO: 60
AT3G61910	SEQ ID NO: 61	SEQ ID NO: 62
AT5G07310	SEQ ID NO: 63	SEQ ID NO: 64
AT3G14230	SEQ ID NO: 65	SEQ ID NO: 66
AT1G28160	SEQ ID NO: 67	SEQ ID NO: 68
AT1G69120	SEQ ID NO: 69	SEQ ID NO: 70
AT3G10490	SEQ ID NO: 71	SEQ ID NO: 72
AT5G61600	SEQ ID NO: 73	SEQ ID NO: 74
AT1G43160	SEQ ID NO: 75	SEQ ID NO: 76

Moreover, examples of a transcription factor that is introduced into a plant or in which a transcriptional regulatory region is modified include transcription factors specified by AGI codes for *Arabidopsis thaliana* listed in tables 3 and 4. In addition, any transcription factor listed in table 3 causes a significant increase in seed protein content when it is introduced into a plant or a transcriptional regulatory region thereof is modified. Any transcription factor listed in table 4 causes a significant decrease in seed protein content when it is introduced into a plant or a transcriptional regulatory region thereof is modified.

TABLE 3

AGI code	Nucleotide sequence	Amino acid sequence
AT3G04070	SEQ ID NO: 77	SEQ ID NO: 78
AT2G46770	SEQ ID NO: 79	SEQ ID NO: 80
AT5G35550	SEQ ID NO: 81	SEQ ID NO: 82

TABLE 4

AGI code	Nucleotide sequence	Amino acid sequence
AT1G10200	SEQ ID NO: 83	SEQ ID NO: 84

In addition, examples of a transcription factor constituting a chimeric protein or a transcription factor subjected to gene introduction or modification of an expression control region are not limited to amino acid sequences (shown in the even-numbered SEQ ID NOS: 1 to 84) listed in tables 1 to 4. Also, it is possible to use a transcription factor having transactivation activity and comprising an amino acid sequence that has a deletion, a substitution, an addition, or an insertion of one or a plurality of amino acid sequences with respect to any of the amino acid sequences. Here, the term “a plurality of amino acids” refers to 1 to 20, preferably 1 to 10, more preferably 1 to 7, further preferably 1 to 5, and particularly preferably 1 to 3 amino acids, for example. In addition, amino acid deletion, substitution, or addition can be performed by modifying a nucleotide sequence encoding any of the above transcription factors by a technique known in the art. Mutation can be introduced into a nucleotide sequence by a known technique such as the Kunkel method or the Gapped duplex method or a method based thereon. For example, mutation is introduced with a mutagenesis kit using site-directed mutagenesis (e.g., Mutant-K or Mutant-G (both are trade names of Takara Bio)) or the like, or a LA PCR in vitro Mutagenesis series kit (trade name, Takara Bio). Also, a mutagenesis method may be: a method using a chemical mutation agent represented by EMS (ethyl methanesulfonate), 5-bromouracil, 2-aminopurine, hydroxylamine, N-methyl-N'-nitro-N nitrosoguanidine, or other carcinogenic compounds; or a method that involves radiation treatment or ultraviolet [UV] treatment typically using X-rays, alpha rays, beta rays, gamma rays, an ion beam, or the like.

Further, examples of a transcription factor constituting a chimeric protein or a transcription factor subjected to gene introduction or modification of an expression control region are not limited to *Arabidopsis thaliana* transcription factors listed in tables 1 to 4. Examples of such transcription factor can include transcription factors that function in a similar manner in non-*Arabidopsis thaliana* plants (e.g., the aforementioned plants) (hereinafter referred to as homologous transcription factors). These homologous transcription factors can be searched for using the genomic information of a search target plant based on amino acid sequences listed in tables 1 to 4 or the nucleotide sequences of individual genes if the plant genomic information has been elucidated. Homologous transcription factors can be identified by searching for amino acid sequences having, for example, 70% or higher, preferably 80% or higher, more preferably 90% or higher, and most preferably 95% or higher homology to the amino acid sequences listed in tables 1 to 4. Here, the value of homology refers to a value that can be found based on default setting using a computer equipped with a BLAST algorithm and a database containing gene sequence information.

In addition, a homologous gene can be identified by, when the plant genome information remains unclarified, extracting the genome from a target plant or constructing a cDNA library for a target plant and then isolating a genomic region or cDNA hybridizing under stringent conditions to at least some portions of the gene encoding any one of the transcription factors listed in tables 1 to 4. Here, the term “stringent conditions” refers to conditions under which namely a specific hybrid is formed, but a non-specific hybrid is never formed. For

example, such conditions comprise hybridization at 45° C. with 6 x SSC (sodium chloride/sodium citrate), followed by washing at 50° C. to 65° C. with 0.2-1 x SSC and 0.1% SDS. Alternatively, such conditions comprise hybridization at 65° C. to 70° C. with 1 x SSC, followed by washing at 65° C. to 70° C. with 0.3 x SSC. Hybridization can be performed by a conventionally known method such as a method described in J. Sambrook et al. Molecular Cloning, A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory (1989).

A feature of causing the seed protein content to vary significantly (to be improved or reduced significantly) is imparted to the plant of the present invention by causing expression of the aforementioned chimeric protein comprising a transcription factor and a functional peptide in a plant, introducing the aforementioned gene encoding a transcription factor into a plant, or altering an expression control region of such gene in a plant.

In particular, a feature of causing the seed protein content to vary significantly (to be improved or reduced significantly) is imparted to the plant of the present invention by causing expression of a chimeric protein comprising a transcription factor of interest having repressed transactivation activity, further causing expression of transcription repression activity through recognition of a cis sequence homologous to a cis sequence recognized by the transcription factor of interest, and altering the specific affinity of the transcription factor of interest to that of another factor, nucleic acid, lipid, or carbohydrate. In the plant of the present invention, it is possible to create a chimeric protein comprising an endogenous transcription factor by modifying the endogenous transcription factor. Alternatively, it is also possible to introduce a gene encoding a chimeric protein into the plant so as to cause the gene to be expressed therein. For instance, it is preferable to use a method wherein a gene encoding a chimeric protein (fusion protein) obtained by fusing the aforementioned transcription factor and a functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor is introduced into a target plant to cause the chimeric protein (fusion protein) to be expressed in the plant.

The expression “transcription factor having repressed transactivation activity” used herein is not particularly limited. Such transcription factor has significantly lower transactivation activity than the original transcription factor. In addition, a “functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor” (sometimes referred to as a “transcription repressor converting peptide”) is defined as a peptide having the function of causing an arbitrary transcription factor to have significantly reduced transactivation activity in comparison with the original transcription factor when the peptide is fused with the transcription factor to create a chimeric protein. Such “functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor” is not particularly limited. However, it is particularly preferable for the functional peptide to consist of an amino acid sequence known as a repressor domain sequence or an SRDX sequence. Examples of such transcription repressor converting peptide are described in detail in JP Patent Publication (Kokai) No. 2005-204657 A. Any example disclosed in such document can be used.

For example, a transcription repressor converting peptide consists of an amino acid sequence expressed by any one of the following formula (1) to (8).

(1) X1-Leu-Asp-Leu-X2-Leu-X3 (SEQ ID NO: 392 with deletion of 0-10 residues from the N-terminus)

(where X1 denotes a set of 0 to 10 amino acid residues, X2 denotes Asn or Glu, and X3 denotes a set of at least 6 amino acid residues.)

(2) Y1-Phe-Asp-Leu-Asn-Y2-Y3 (SEQ ID NO: 393 with deletion of 0-10 residues from the N-terminus)

(where Y1 denotes a set of 0 to 10 amino acid residues, Y2 denotes Phe or Ile, and Y3 denotes a set of at least 6 amino acid residues.)

(3) Z1-Asp-Leu-Z2-Leu-Arg-Leu-Z3 (SEQ ID NO: 394 with deletion of 0-10 residues from the C-terminus and deletion of 0-2 residues from the N-terminus)

(where Z1 denotes Leu, Asp-Leu, or Leu-Asp-Leu, Z2 denotes Glu, Gln, or Asp, and Z3 denotes a set of 0 to 10 amino acid residues.)

(4) Asp-Leu-Z4-Leu-Arg-Leu (residues 4-9 of SEQ ID NO: 394)

(where Z4 denotes Glu, Gln, or Asp.)

(5) $\alpha 1$ -Leu- $\beta 1$ -Leu- $\gamma 1$ -Leu (SEQ ID NO: 395)

(6) $\alpha 1$ -Leu- $\beta 1$ -Leu- $\gamma 2$ -Leu (SEQ ID NO: 396)

(7) $\alpha 1$ -Leu- $\beta 2$ -Leu-Arg-Leu (SEQ ID NO: 397)

(8) $\alpha 2$ -Leu- $\beta 1$ -Leu-Arg-Leu (SEQ ID NO: 398)

(where $\alpha 1$ denotes Asp, Asn, Glu, Gln, Thr, or Ser, $\alpha 2$ denotes Asn, Glu, Gln, Thr, or Ser, $\beta 1$ denotes Asp, Gln, Asn, Arg, Glu, Thr, Ser, or His, $\beta 2$ denotes Asn, Arg, Thr, Ser, or His, $\gamma 1$ denotes Arg, Gln, Asn, Thr, Ser, His, Lys, or Asp, and $\gamma 2$ denotes Gln, Asn, Thr, Ser, His, Lys, or Asp in formulae (5) to (8).)

Transcription repressor converting peptide of formula (1)

The number of amino acid residues in the set denoted by "X1" may be 0 to 10 for the transcription repressor converting peptide of formula (1). In addition, types of specific amino acids corresponding to amino acid residues in the set denoted by X1 are not particularly limited. Any amino acid can be used. In view of ease of synthesis of the transcription repressor converting peptide of formula (1), it is preferable to minimize the length of the set of amino acid residues denoted by X1. Specifically, the number of amino acid residues in the set denoted by X1 is preferably not more than 5.

Similarly, the number of amino acid residues in the set denoted by X3 may be at least 6 for the transcription repressor converting peptide of formula (1). In addition, types of specific amino acids corresponding to amino acid residues in the set denoted by X3 are not particularly limited, and thus any amino acid may be used.

Transcription Repressor Converting Peptide of Formula (2)

As in the case of X1 for the transcription repressor converting peptide of formula (1), the number of amino acid residues in the set denoted by Y1 for the transcription repressor converting peptide of formula (2) may be 0 to 10. In addition, types of specific amino acids corresponding to amino acid residues in the set denoted by Y1 are not particularly limited, and thus any amino acid may be used. The number of specific amino acid residues in the set denoted by Y1 is preferably not more than 5.

Similarly, as in the case of X3 for the transcription repressor converting peptide of formula (1), the number of amino acid residues in the set denoted by Y3 for the transcription repressor converting peptide of formula (2) may be at least 6. In addition, types of specific amino acids corresponding to amino acid residues in the set denoted by Y3 are not particularly limited, and thus any amino acid may be used.

Transcription Repressor Converting Peptide of Formula (3)

For the transcription repressor converting peptide of formula (3), the set of amino acid residues denoted by Z1 contains 1 to 3 "Leu" amino acids. When it contains a single amino

acid, Z1 denotes Leu. When it contains two amino acids, Z1 denotes Asp-Leu. When it contains 3 amino acids, Z1 denotes Leu-Asp-Leu.

Meanwhile, for the transcription repressor converting peptide of formula (3), the number of amino acid residues in the set denoted by Z3 may be 0 to 10. In addition, types of specific amino acids corresponding to amino acid residues in the set denoted by Z3 are not particularly limited, and thus any amino acid may be used. Specifically, the number of amino acid residues in the set denoted by Z3 is preferably not more than 5. Specific examples of an amino acid residue in the set denoted by Z3 include, but are not limited to, Gly, Gly-Phe-Phe, Gly-Phe-Ala, Gly-Tyr-Tyr, and Ala-Ala-Ala.

In addition, the number of amino acid residues consisting of a transcription repressor converting peptide as a whole of formula (3) is not particularly limited. However, in view of ease of synthesis, it is preferably not more than 20 amino acids.

Transcription Repressor Converting Peptide of Formula (4)

The transcription repressor converting peptide of formula (4) is a hexamer (6mer) consisting of 6 amino acid residues. In addition, if the amino acid residue denoted by Z4 in the transcription repressor converting peptide of formula (4) is Glu, the amino acid sequence of the peptide corresponds to a region ranging from position 196 to position 201 of the amino acid sequence of the *Arabidopsis thaliana* SUPERMAN protein (SUP protein).

A chimeric protein (fusion protein) is created through fusion of any of the different transcription repressor converting peptides described above and any of the transcription factors described above so as to modify characteristics of the transcription factor. Specifically, a chimeric protein (fusion protein) is created through fusion of the transcription factor and the transcription repressor converting peptide, making it possible to modify the transcription factor into a transcriptional repressor or a negative transcriptional coactivator. In addition, it is possible to further convert a non-dominant transcriptional repressor into a dominant transcriptional repressor.

In addition, a chimeric protein (fusion protein) can be produced by obtaining a fusion gene of a polynucleotide encoding any transcription repressor converting peptide described above and a gene encoding a transcription factor. Specifically, a fusion gene is constructed by linking a polynucleotide encoding the transcription repressor converting peptide (hereinafter referred to as a "transcription repressor converting polynucleotide") and the gene encoding a transcription factor. The fusion gene is introduced into plant cells, thereby allowing production of a chimeric protein (fusion protein). The specific nucleotide sequence of the transcription repressor converting polynucleotide is not particularly limited. It is only necessary for the transcription repressor converting polynucleotide to comprise a nucleotide sequence corresponding to the amino acid sequence of the transcription repressor converting peptide in accordance with the genetic code of the peptide. In addition, if necessary, the transcription repressor converting polynucleotide may have a nucleotide sequence that serves as a linking site via which the transcription repressor converting polynucleotide is linked to a transcription factor gene. Further, if the amino acid reading frame of the transcription repressor converting polynucleotide does not match the reading frame of the transcription factor gene, the transcription repressor converting polynucleotide can comprise an additional nucleotide sequence that allows matching of both reading frames. Furthermore, the transcription repressor converting polynucleotide may comprise a variety of additional polypeptides such as a polypeptide hav-

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ing a linker function to link a transcription factor and a transcription repressor converting peptide and a polypeptide such as His, Myc, or Flag used for epitope labeling of a chimeric protein (fusion protein). Moreover, if necessary, the chimeric protein (fusion protein) may have a construct such as a sugar chain, an isoprenoid group, or the like as well as such polypeptide.

In addition, a conventionally known expression vector or the like can be used when the above gene encoding a transcription factor is introduced into plants.

A method for producing a plant is not particularly limited as long as it comprises a step of producing the above chimeric protein comprising a transcription factor and a transcription repressor converting peptide in a plant or a step of introducing the above gene encoding a transcription factor into a plant or modifying an expression control region of the gene. However, for example, a production method comprising steps such as an expression vector construction step, a transformation step, and a selection step can be used. Each step is specifically described below.

Expression Vector Construction Step

The expression vector construction step is not particularly limited as long as it includes a step of constructing a recombinant expression vector containing the gene encoding a transcription factor, a transcription repressor converting polynucleotide, and a promoter. Also, the expression vector construction step is not particularly limited as long as it is a step of constructing a recombinant expression vector containing the gene encoding a transcription factor to be introduced and a promoter. As a vector serving as a mother body for a recombinant expression vector, various conventionally known vectors can be used. For example, plasmids, phages, cosmids, or the like can be used and such vector can be appropriately selected depending on plant cells into which it is introduced and introduction methods. Specific examples of such vector include pBR322, pBR325, pUC19, pUC119, pBluescript, pBluescriptSK, and pBI vectors. Particularly, when a method for introduction of a vector into a plant uses *Agrobacterium*, a pBI binary vector is preferably used. Specific examples of such pBI binary vector include pBIG, pBIN19, pBI101, pBI121, and pBI221.

A promoter used herein is not particularly limited as long as it can cause gene expression in plants. Any known promoter can be appropriately used. Examples of such promoter include a cauliflower mosaic virus 35S promoter (CaMV35S), various actin gene promoters, various ubiquitin gene promoters, a nopaline synthase gene promoter, a tobacco PR1a gene promoter, a tomato ribulose1,5-bisphosphate carboxylase-oxidase small subunit gene promoter, a napin gene promoter, and an oleosin gene promoter. Of these, a cauliflower mosaic virus 35S promoter, an actin gene promoter, or a ubiquitin gene promoter can be more preferably used. The use of each of the above promoters enables strong expression of any gene when it is introduced into plant cells. The structure of a recombinant expression vector itself is not particularly limited as long as the promoter is linked to a fusion gene obtained by linking a gene encoding a transcription factor and a transcription repressor converting polynucleotide so as to cause expression of the gene and introduced into the vector. Also, the structure of a recombinant expression vector itself is not particularly limited as long as the promoter is linked to a gene encoding a desired transcription factor for gene introduction so as to cause expression of the gene and introduced into the vector.

In addition, a recombinant expression vector may further contain other DNA segments, in addition to a promoter and the fusion gene or the gene encoding a transcription factor.

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Such other DNA segments are not particularly limited and examples thereof include a terminator, a selection marker, an enhancer, and a nucleotide sequence for enhancing translation efficiency. Also, the above recombinant expression vector may further have a T-DNA region. A T-DNA region can enhance efficiency for gene introduction particularly when the above recombinant expression vector is introduced into a plant using *Agrobacterium*.

A transcription terminator is not particularly limited as long as it has functions as a transcription termination site and may be any known transcription terminator. For example, specifically, a transcription termination region (Nos terminator) of a nopaline synthase gene, a transcription termination region (CaMV35S terminator) of cauliflower mosaic virus 35S, or the like can be preferably used. Of them, the Nos terminator can be more preferably used. In the case of the above recombinant vector, a phenomenon such that an unnecessarily long transcript is synthesized and that a strong promoter decreases the number of copies of a plasmid after introduction into plant cells can be prevented by arranging a transcription terminator at an appropriate position.

As a transformant selection marker, a drug resistance gene can be used, for example. Specific examples of such drug resistance gene include drug resistance genes against hygromycin, bleomycin, kanamycin, gentamicin, chloramphenicol, and the like. Transformed plants can be easily selected by selecting plants that can grow in medium containing the above antibiotics.

An example of a nucleotide sequence for increasing translation efficiency is an omega sequence from tobacco mosaic virus. This omega sequence is arranged in an untranslated region (5'UTR) of a promoter, so that the translation efficiency of the fusion gene can be increased. As such, the recombinant expression vector can contain various DNA segments depending on purposes.

A method for constructing a recombinant expression vector is not particularly limited. To an appropriately selected vector serving as a mother body, the above promoter, a fusion gene consisting of a gene encoding a transcription factor and a transcription repressor converting polynucleotide or a gene encoding a desired transcription factor for gene introduction, and, if necessary, the above other DNA segments may be introduced in a predetermined order. For example, a gene encoding a transcription factor and a transcription repressor converting polynucleotide are linked to construct a fusion gene, and then the fusion gene and the promoter (e.g., a transcription terminator according to need) are then linked to construct an expression cassette and then the cassette may be introduced into a vector.

In construction of a chimeric gene (fusion gene) and an expression cassette, for example, cleavage sites of DNA segments are prepared to have protruding ends complementary to each other and then performing a reaction with a ligation enzyme, making it possible to specify the order of the DNA segments. In addition, when an expression cassette contains a terminator, DNA segments may be arranged in the following order from upstream: a promoter, the fusion gene or the gene encoding a transcription factor, and a terminator. Also, reagents for construction of an expression vector (that is, types of restriction enzymes, ligation enzymes, and the like) are also not particularly limited. Hence, commercially available reagents can be appropriately selected and used.

Also, a method for replicating (a method for producing) the above expression vector is not particularly limited and conventionally known replication methods can be used herein. In general, such expression vector may be replicated within

Escherichia coli as a host. At this time, preferred types of *Escherichia coli* may be selected depending on the types of vector.

Transformation Step

The transformation step carried out in the present invention is a step of introducing the fusion gene or the gene encoding a transcription factor into plant cells using the above recombinant expression vector so as to cause the expression of the gene. A method for introducing such gene into plant cells (transformation method) using a recombinant expression vector is not particularly limited. Conventionally known appropriate introduction methods can be used depending on plant cells. Specifically, a method using *Agrobacterium* or a method that involves direct introduction into plant cells can be used, for example. As a method using *Agrobacterium*, a method described in the following can be employed, for example: Bechtold, E., Ellis, J. and Pelletier, G. (1993), In *Planta Agrobacterium-mediated gene transfer by infiltration of adult *Arabidopsis* plants*. C. R. Acad. Sci. Paris Sci. Vie, 316, 1194-1199; or Zyprian E., Kado Cl, *Agrobacterium-mediated plant transformation by novel mini-T vectors in conjunction with a high-copy vir region helper plasmid*, Plant Molecular Biology, 1990, 15(2), 245-256.

As a method for directly introducing DNA comprising a recombinant expression vector and a target gene into plant cells, microinjection, electroporation, a polyethylene glycol method, a particle gun method, protoplast fusion, a calcium phosphate method, or the like can be employed.

Also, when a method for directly introducing DNA into plant cells is employed, DNA that can be used herein contains transcriptional units required for the expression of a target gene, such as a promoter and a transcription terminator, and a target gene. Vector functions are not essential in such case. Moreover, a DNA that contains a protein coding region alone of a target gene having no transcriptional unit may be used herein, as long as it is integrated into a host's transcriptional unit and then the target gene can be expressed.

Examples of plant cells into which DNA comprising the above recombinant expression vector and a target gene or DNA containing no expression vector but a target gene DNA is introduced include cells of each tissue of plant organs such as flowers, leaves, and roots, calluses, and suspension-cultured cells. At this time, according to the plant production method of the present invention, an appropriate expression vector may be constructed as the above recombinant expression vector according to the type of plant to be produced or a versatile expression vector may be constructed in advance and then introduced into plant cells. That is to say, the plant production method of the present invention may or may not comprise a step of constructing a DNA for transformation using the recombinant expression vector.

Other Steps and Methods

The plant production method of the present invention needs to comprise at least the transformation step, and the method may further comprise a step of constructing the DNA for transformation using the recombinant expression vector. The method may further comprise other steps. Specifically, for example, a step of selecting an appropriate transformant from among transformed plants can be employed.

A selection method is not particularly limited. For example, selection may be carried based on drug resistance such as hygromycin resistance. Alternatively, selection may be carried out based on the protein content in plant seeds collected from cultivated transformants. For example, a method comprising collecting plant seeds, determining the protein content in the seeds according to a standard method, and comparing the protein content with the protein content in

non-transformed plant seeds can be employed in a case in which selection is carried out based on protein content (see the Examples described below).

According to the plant production method of the present invention, the fusion gene or the gene encoding a transcription factor is introduced into a plant. This makes it possible to obtain an offspring plant having a significantly improved or reduced protein content in comparison with the plant via sexual reproduction or asexual reproduction. Also, plant cells or reproductive materials, such as seeds, fruits, stocks, calluses, tubers, cut ears, or lumps, may be obtained from the plant or an offspring plant thereof. The plant can be mass-produced therefrom based on such materials. Therefore, the plant production method of the present invention may comprise a reproduction step (mass production step) for reproducing a selected plant.

In addition, the plant of the present invention may include a matter comprising at least any one of an adult plant, plant cells, plant tissue, callus, and seeds. That is, according to the present invention, any matter in a state that allows it to eventually grow to become a plant can be regarded as a plant. In addition, plant cells include plant cells in various forms. Examples of such plant cells include suspension-cultured cells, protoplasts, and leaf sections. As a result of proliferation/differentiation of such plant cells, a plant can be obtained. In addition, a plant can be reproduced from plant cells by a conventionally known method depending on the types of plant cells. Therefore, the plant production method of the present invention may comprise a regeneration step of regenerating a plant from plant cells or the like.

In addition, the plant production method of the present invention is not limited to a method of transformation using a recombinant expression vector. A different method may be used. Specifically, for example, the chimeric protein (fusion protein) itself or a transcription factor (protein) can be administered to a plant. In this case, the chimeric protein (fusion protein) or a transcription factor (protein) can be administered to a young plant such that the seed protein content can be improved. In addition, a method of administration of a chimeric protein (fusion protein) or a transcription factor (protein) is not particularly limited, and a different known method can be used.

As described above, according to the present invention, it becomes possible to provide a plant for which the seed protein content has been caused to vary significantly (to be improved or reduced significantly) relative to the protein content in a wild-type plant by inducing expression of a chimeric protein comprising a predetermined transcription factor and any functional peptide described above or a predetermined transcription factor. When the chimeric protein is expressed in a plant, it might cause repression of transactivation activity of a target transcription factor or it might cause exhibition of transcription repression effects upon a sequence homologous to a cis sequence recognized by a target transcription factor. Further, in some cases, such chimeric protein functions to change the specific affinity of another factor, DNA, RNA, lipid, or carbohydrate having affinity to a target transcription factor or transcriptional coactivator. Alternatively, in some cases, it functions to cause a substance having no affinity to a target transcription factor to have improved affinity thereto. The following factors can be expressed in a similar manner in the plant of the present invention: a transcription factor that constitutes a chimeric protein; a transcription factor capable of recognizing a cis sequence homologous to a cis sequence recognized by the transcription factor; a transcription factor homologous to a transcription factor that constitutes a chimeric protein; other factors each having affinity to a transcrip-

tion factor that constitutes a chimeric protein; and the like. However, the above effects of a chimeric protein allow suppression of gene expression to be controlled in a dominant-negative manner. Accordingly, the expression levels of gene groups involved in plant growth and the expression levels of gene groups involved in protein production in seeds and/or gene groups involved in decomposition of a produced protein would vary in the plant of the present invention. This is thought to cause significant variation in seed protein content.

Here, significant variation in the seed protein content exists in a case in which the plant of the present invention exhibits an improvement of the protein amount over a wild-type plant while the single seed mass remains stable, a case in which the plant of the present invention is found to exhibit improvement of protein content with a significantly higher or lower level of single seed mass than that of a wild-type plant, or a case in which the plant of the present invention is found to exhibit improvement or reduction of seed protein content when compared with a wild-type plant. In any case, it corresponds to a variation in the amount of a protein produced by a single individual plant.

More specifically, if a chimeric protein comprising any transcription factor listed in table 1 is expressed in a plant, the protein content in seeds of the plant would be improved by approximately 20% or more compared with a wild-type plant. In addition, if a gene encoding any transcription factor listed in table 3 is introduced into a plant, the protein content in seeds of the plant would be improved by approximately 20% or more compared with a wild-type plant. Among the plants of the present invention, a plant confirmed to have increased protein content can be used for a method for producing a plant-derived protein. For example, a protein can be produced by cultivating the plant of the present invention, taking seeds therefrom, and collecting protein components from the obtained seeds. In particular, it can be said that the protein production method using the plant of the present invention is a method whereby high protein content in seeds can be achieved, resulting in excellent productivity. In other words, assuming that the number of cultivated plant individuals per unit area of cultivated acreage is stable and thus the amount of collected seeds is stable, the amount of protein produced per unit area of cultivated acreage can be remarkably improved with the use of the plant of the present invention. Therefore, production cost necessary for protein production can be significantly reduced with the use of the plant of the present invention.

EXAMPLES

The present invention is hereafter described in greater detail with reference to the following examples, although the technical scope of the present invention is not limited thereto.

Example 1

Transcription Factor Gene Amplification

Each of the following transcription factors was subjected to PCR amplification of a coding region DNA fragment including or excluding a termination codon using the *Arabidopsis thaliana* cDNA library and primers described below:

At2g23760,	At1g18330,	At2g02070,	At1g12980,
At5g62380,	At4g23750,	At4g32800,	At1g24590,
At5g07690,	At1g71692,	At1g52150,	At3g25890,
At1g09540,	At5g22380,	At2g44940,	At5g41030,
At5g60970,	At5g35550,	At1g60240,	At2g23290,
At5g14000,	At1g19490,	At5g58900,	At5g07580,
At3g04070,	At2g42830,	At2g22200,	At5g25190,
At5g54230,	At5g67300,	At4g28140,	At5g23260,
At1g69490,	At4g18390,	At1g15360,	At1g27370,
At1g78080,	At5g25390,	At3g04060,	At1g44830,
At3g49850,	At5g06100,	At1g74840,	At3g04070,
At2g46770,	At5g35550,	At1g71030,	At2g44840,
At3g23220,	At1g18570,	At3g01530,	At5g51190,
At1g434410,	At5g22290,	At3g04420,	At3g45150,
At3g29035,	At3g02150,	At2g41710,	At1g49120,
At1g64380,	At3g23230,	At1g01010,	At5g53290,
At1g36060,	At5g66300,	At2g46310,	At5g47390,
At1g71030,	At1g17520,	At3g23220,	At2g18060,
At5g08070,	At1g80580,	At1g34190,	At2g47520,
At5g67000,	At1g27950,	At5g47230,	At3g28910,
At5g11280,	At5g07680,	At1g25470,	At1g28520,
At1g77450,	At5g24590,	At5g08790,	At1g67260,
At4g28530,	At5g13910,	At5g64530,	At2g33710,
At1g53230,	At1g56010,	At5g18560,	At5g67580,
At5g24520,	At4g18390,	At1g69690,	At5g13330,
At5g60970,	At3g23220,	At1g62700,	At5g13330,
At1g22985,	At5g09330,	At1g10200,	At1g61110,
At1g30210,	At5g40330,	At5g13180,	At1g52880,
At4g18450,	At5g07580,	At1g74930,	At4g36160,
At3g18550,	At5g64750,	At2g02450,	At2g42400,
At5g67300,	At1g68800,	At1g14510,	At1g25580,
At5g18270,	At2g44840,	At3g15500,	At4g35580,
At4g01550,	At4g37750,	At1g52890,	At2g17040,
At2g33480,	At5g39610,	At1g32770,	At5g47220,
At1g56650,	At1g63910,	At3g15510,	At2g45680,
At2g31230,	At1g12260,	At3g61910,	At5g07310,
At3g14230,	At1g28160,	At1g69120,	At3g10490,
At5g61600,	At1g43160,	At3g15210,	At4g08150,
At1g10200,			and At1g10200. Note that a coding region DNA fragment including a termination codon was amplified for each of At3g04070, At2g46770, At5g35550, At1g71030, At2g44840, At4g18390, At1g69690, At5g13330, At5g60970, At3g23220, At3g15210, At4g08150, and At1g10200. PCR was carried out under conditions of 94° C. for 1 minute, 47° C. for 2 minutes, and elongation reaction at 74° C. for 1 minute for 25 cycles. Next, each PCR product was isolated by agarose gel electrophoresis and collected.

TABLE 5

AGI code	Forward primer	Nucleotide sequence	Reverse primer	Nucleotide sequence
At2g23760	GATGGGTTAGCTACTACAACCTTCTTCTAT	SEQ ID NO: 85	AAAAATCTCCAAAGTCCTCTAACGGAGAAAGA	SEQ ID NO: 86
At1g18330	GATGCCCGCTGAGGATCGAAGTGAGGAACCT	SEQ ID NO: 87	GCATATACGTGCTCTTGGCTTTCTTTTC	SEQ ID NO: 88
At2g02070	GATGGCTGCTCTTCATCCTCCGCTGCTTC	SEQ ID NO: 89	GAAACTCGCATGATGGATTCCATAAGGTGG	SEQ ID NO: 90
At1g12980	AATGGAAAAAGCCTTGAGAACTTC	SEQ ID NO: 91	TCCCCACGATCTCGGCAAGTACA	SEQ ID NO: 92
At5g62380	GATGGAAAGTCTCGCACACATTCCCTCCCGG	SEQ ID NO: 93	CGTGTGTATTTGAGCCCAAGAGTAGAA	SEQ ID NO: 94

TABLE 5-continued

AGI code	Forward primer	Nucleotide sequence	Reverse primer	Nucleotide sequence
At4g23750	ATGGAAGCGGAGAAGAAAATGG	SEQ ID NO: 95	AACAGCTAAAAGAGGGATCCGAC	SEQ ID NO: 96
At4g32800	ATGGCGGATTCTGCTTCCGAC	SEQ ID NO: 97	GGGAAAATGTTCCAAGATTTCG	SEQ ID NO: 98
At1g24590	ATGGAAGAACCAATCATGAGAC	SEQ ID NO: 99	ATAATCATCATGAAAGCAATACTG	SEQ ID NO: 100
At5g07690	GATGTCAAGAACGCCATGTTGTGAGAGA	SEQ ID NO: 101	TATGAAGTTCTTGCGTCGTAATCTGGCT	SEQ ID NO: 102
At1g71692	GATGGCTCGTGGAAAGATTCAAGCTTAAGAG	SEQ ID NO: 103	GAACTGAAATATTCACTTGGCATTGTTAG	SEQ ID NO: 104
At1g52150	GATGGCAATGTCCTGCAAGGATGGTAAGTT	SEQ ID NO: 105	CACAAAGGCCAATTGATGAACACAAAGCA	SEQ ID NO: 106
At3g25890	ATGGCTGAACGAAAGAACACGC	SEQ ID NO: 107	TGGGCACGCGATATTAAGAGG	SEQ ID NO: 108
At1g09540	GATGGGGAGACATTCTGCTGTTACAAACA	SEQ ID NO: 109	AAGGGACTGACCAAAAGAGACGGCCATTCT	SEQ ID NO: 110
At5g22380	GATGGCCGATGAGGTACAATCGGTTTCG	SEQ ID NO: 111	AGGCCAAGTCAGCTGTTCCCAGTCCCACAT	SEQ ID NO: 112
At2g44940	ATGGCAAGACAAATCAACATAGAG	SEQ ID NO: 113	TTCAGATAGAAAAAACGGCTCTTC	SEQ ID NO: 114
At5g41030	ATGGTCATGGAGGCCAAGAAG	SEQ ID NO: 115	TGAACCATTTCCTCTGCACCTC	SEQ ID NO: 116
At5g60970	ATGAGATCAGGAGAATGTGATG	SEQ ID NO: 117	AGAATCTGATTCAATTATCGCTAC	SEQ ID NO: 118
At5g35550	GATGGAAAGAGAGCAACTACTAGTGTGAG	SEQ ID NO: 119	ACAAGTGAAGTCTCGGAGCCAATCTTCATC	SEQ ID NO: 120
At1g60240	GATGAAGTCAAGACGTGAAACATCAATCGA	SEQ ID NO: 121	TTTATAGTAACCTCGAATGTGCTGGCCAA	SEQ ID NO: 122
At2g23290	GATGTCTGGTCGACCCGGAAAGAAATGGA	SEQ ID NO: 123	CTCGATCCTACCTAACCAATAAACTCTCT	SEQ ID NO: 124
At5g14000	GATGGAGGTGGAGAAGAGGATTGTAG	SEQ ID NO: 125	CTCATCAGCTGAGGTAGGAGGAG	SEQ ID NO: 126
At1g19490	GATGGAGTTGGAGCCTATATCATCGAGTTG	SEQ ID NO: 127	TCCGACCTGCATCCGACATTGACGGCCATG	SEQ ID NO: 128
At5g58900	GATGGAGGTTATGAGACCGTCGACGTACAC	SEQ ID NO: 129	TAGTTGAAACATTGTGTTTGGCGTCATA	SEQ ID NO: 130
At5g07580	ATGGCGAGTTTGAGGAAAGC	SEQ ID NO: 131	AAATGCATCACAGGAAGATGAAG	SEQ ID NO: 132
At3g04070	GATGATAAGCAAGGATCCAAGATCGAGTTT	SEQ ID NO: 133	GCCTTGATATTGAGGTTGAGAACTCATCAT	SEQ ID NO: 134
At2g42830	GATGGAGGGTGGTGCAGTAATGAAGTAGC	SEQ ID NO: 135	AAACAGTTGCAGAGGTGGTTGGCTTGGTT	SEQ ID NO: 136
At2g22200	ATGGAAACTGCTCTCTTCTT	SEQ ID NO: 137	AGAATTGGCAGTTACTAACATTGC	SEQ ID NO: 138
At5g25190	ATGGCACGACCACAAACACGC	SEQ ID NO: 139	CAGCGTCTGAGTTGGTAAACAG	SEQ ID NO: 140
At5g54230	GATGGAAAATCTCAAGCTCGGAGGAAAG	SEQ ID NO: 141	TGATAGATTCAAAGCATTATTATGATC	SEQ ID NO: 142
At5g67300	GATGGCTGATAGGATCAAAGGTCATGGAG	SEQ ID NO: 143	CTCGATTCTCCAACTCCAATTGACTCAT	SEQ ID NO: 144
At4g28140	ATGGACTTTGACGAGGAGCTAAATC	SEQ ID NO: 145	AAAGAAAGGCCTCATAGGACAAG	SEQ ID NO: 146
At5g23260	GATGGTAGAGGAAAGATAGAGATAAGAA	SEQ ID NO: 147	ATCATTCTGGGCGGTGATCGTTTGAAAG	SEQ ID NO: 148
At1g69490	GATGGAAGTAACCTCCAATCTACCCCTCCC	SEQ ID NO: 149	AAACTTAAACATCGCTTGACGATGATGGTT	SEQ ID NO: 150
At4g18390	ATGATTGGAGATCTAATGAAG	SEQ ID NO: 151	GTTCTTGCCCTTACCCCTATG	SEQ ID NO: 152
At1g15360	ATGGTACAGACGAGAAGATTTCAG	SEQ ID NO: 153	GTTTGTATTGAGAAGCTCTCTATC	SEQ ID NO: 154
At1g27370	GATGGACTGCAACATGGTATCTCGTCCC	SEQ ID NO: 155	GATGAAATGACTAGGGAAAGTGCCAAATAT	SEQ ID NO: 156
At1g78080	GATGGCAGCTGCTATGAATTGTCAC	SEQ ID NO: 157	AGCTAGAACATCGAACATCCAAATCG	SEQ ID NO: 158
At5g25390	ATGGTACATTGAGAAGATTCCG	SEQ ID NO: 159	GACCTGTGCAATGGATCCAG	SEQ ID NO: 160
At3g04060	GATGGTGGAGAAGAGCGCGCTAG	SEQ ID NO: 161	GCTAGTATATAATCTCCAGAAG	SEQ ID NO: 162
At1g44830	ATGGTAAAACACTTCAAAAGACAC	SEQ ID NO: 163	GCAGAAGTTCCATACTGATATC	SEQ ID NO: 164
At3g49850	GATGGGAGCTCCAAAGCTGAAGTGGACACC	SEQ ID NO: 165	CCGAGTTGGCTATGCAATTCTATACCTCAC	SEQ ID NO: 166
At5g06100	GATGAGTTACAGCAGCACTGACAGTGCACCA	SEQ ID NO: 167	ACAAACTATTCAAGTGTGGTAAGGTGAA	SEQ ID NO: 168
At1g74840	GATGGCCGACGGTAGTACTAGTTCTCGGA	SEQ ID NO: 169	AGCGACTCCAATCGTGTGAATGCTGGATG	SEQ ID NO: 170

TABLE 5-continued

AGI code	Forward primer	Nucleotide sequence	Reverse primer	Nucleotide sequence
At3g04070	GATGATAAGCAAGGATCCAAGATCGAGTTT	SEQ ID NO: 171 CTAGCCTTGATATTGAAGGTGAGAAGTCAT		SEQ ID NO: 172
At2g46770	GATGATGTCAAATCTATGAGCATATC	SEQ ID NO: 173 TTATCCACTACCATTGACACGTGACAAAA		SEQ ID NO: 174
At5g35550	GGGATGGAAAGAGAGCAACTACTAGTGTGAGG	SEQ ID NO: 175 TCAACAAGTGAAGTCTCGGAGCCAATCTTC		SEQ ID NO: 176
At1g71030	GATGAACAAAACCCGCCTTCGTGCTCTCTC	SEQ ID NO: 177 TCATCGGAATAGAAGAACGTTCTGACC		SEQ ID NO: 178
At2g44840	ATGAGCTCATCTGATTCCGTTAATAAC	SEQ ID NO: 179 TTATATCCGATTATCAGAATAAGAAC		SEQ ID NO: 180
At3g23220	ATGAAATACAGAGCGTACGAAAG	SEQ ID NO: 181 GCGGTTGCGTCGTTACAATTG		SEQ ID NO: 182
At1g18570	GATGGTGCACACCGTGTGCAAAGCTGA	SEQ ID NO: 183 TCCAAAATAGTTATCAATTCTGCAAACAA		SEQ ID NO: 184
At3g01530	GATGGAGACGACGATGAAGAAGAAAGGGAG	SEQ ID NO: 185 AATCACATGGTGGTACCCATTAAGCAAGTG		SEQ ID NO: 186
At5g51190	ATGGCTTCTTCACATCAACAAACAG	SEQ ID NO: 187 AGTAACATACGAGTTGAGAGTGTC		SEQ ID NO: 188
At4g34410	ATGCATTATCCTAACACAGAAC	SEQ ID NO: 189 CTGGAACATATCAGCAATTGTATTTC		SEQ ID NO: 190
At5g22290	GATGGACACGAAAGCGGTTGGAGTTTC	SEQ ID NO: 191 TTCTAGATAAAACACATTGCTATC		SEQ ID NO: 192
At3g04420	GATGGAGAATCCGGTGGGTTAAG	SEQ ID NO: 193 TGTTCTTGAGATAGAAGAACATTGG		SEQ ID NO: 194
At3g45150	ATGGATTCGAAAAATGGAATTAAC	SEQ ID NO: 195 AACTGTGGTTGTGGCTGTTGTTG		SEQ ID NO: 196
At3g29035	GATGGATTACAAGGTATCAAGAAC	SEQ ID NO: 197 GAATTCCAACAGCAATCAAGATTTC		SEQ ID NO: 198
At3g02150	ATGAATATCGTCTCTGGAAAGATG	SEQ ID NO: 199 TCACATATGGTGTACACTCCCTACTTG		SEQ ID NO: 200
At2g41710	GATGGCGTCGGTGTGTCGTC	SEQ ID NO: 201 TTCTCTGTGGGGAGTAGCTG		SEQ ID NO: 202
At1g49120	ATGATCAGTTCAGAGAACAGAAC	SEQ ID NO: 203 TAAAAACTTATCGATCCAATCAGTAG		SEQ ID NO: 204
At1g64380	ATGGAAGAAAGCAATGATATTTTC	SEQ ID NO: 205 ATTGGCAAGAACCTCCAAATCAG		SEQ ID NO: 206
At3g23230	ATGGAGAGCTAAACAGGAGC	SEQ ID NO: 207 TCTCTCCTTCTCTGAATCAAG		SEQ ID NO: 208
At1g01010	GATGGAGGATCAAGTTGGGTTGG	SEQ ID NO: 209 ACCAACAGAACATGATCCAACATAATG		SEQ ID NO: 210
At5g53290	ATGGACGAATATATTGATTCCGAC	SEQ ID NO: 211 AGCAACTAATAGATCTGATATCAATG		SEQ ID NO: 212
At1g36060	ATGGCGGATCTTCGGTGG	SEQ ID NO: 213 CGATAAAATTGAAAGCCCAATCTATC		SEQ ID NO: 214
At5g66300	GATGATGAAGGTTGATCAAGATTATCGTG	SEQ ID NO: 215 GTCTTCTCCACTCATCAAAATTGAGACGC		SEQ ID NO: 216
At2g46310	ATGAAAAGCCGAGTGAGAAATC	SEQ ID NO: 217 TTACTTATCCAACAAATGATCTGG		SEQ ID NO: 218
At5g47390	GATGACTCGCGATGTTCTCACTGCAATCA	SEQ ID NO: 219 TAAAGCGTGTATCACGCTTTGATGTCTGA		SEQ ID NO: 220
At1g71030	GATGAACAAAACCCGCCTTCGTGCTCTC	SEQ ID NO: 221 TCGGAATAGAAGAACGTTCTGACCTGT		SEQ ID NO: 222
At1g17520	GATGGAAATCAGAACGCTCAAATGGACGGC	SEQ ID NO: 223 ATTCAAGTACATAATCTTCCCCTGACTACA		SEQ ID NO: 224
At3g23220	GATGGATCCATTAACTCAGTCCCCATT	SEQ ID NO: 225 CCAAGTCCCCTATTTTCAAGAACCCCCAA		SEQ ID NO: 226
At2g18060	GATGGAGCAATGGAATCTGTAGCGTTCC	SEQ ID NO: 227 ATTATCAAATACGCAAATCCCAATATCATA		SEQ ID NO: 228
At5g08070	ATGGGAATAAAAAGAAGATCAG	SEQ ID NO: 229 CTCGATATGGTCTGGTTGTGAG		SEQ ID NO: 230
At1g80580	ATGGAAAACAGCTACACCGTTG	SEQ ID NO: 231 CTTCTCTAGACAACAAACCTAAAC		SEQ ID NO: 232
At1g34190	GATGGCGGATTCTCACCGATTC	SEQ ID NO: 233 GTCTTCAAGAGAACGACTTCTACC		SEQ ID NO: 234
At2g47520	ATGTGTGGGGAGCTATCATTTC	SEQ ID NO: 235 ATTGGAGTCTGATAGCTCC		SEQ ID NO: 236
At5g67000	ATGGATAATTCAAGAAAATGTTC	SEQ ID NO: 237 TCTCCACCGCCGTTAATTG		SEQ ID NO: 238
At4g27950	ATGATGATGGATGAGTTATGGATC	SEQ ID NO: 239 CACAAGTAAAGAGATCGGATATC		SEQ ID NO: 240
At5g47230	GGGGATGGCGACTCTAACGAAGT	SEQ ID NO: 241 AACAAACGGTCAACTGGAAATAACCAACG		SEQ ID NO: 242
At3g28910	GATGGTGAGGCCCTTGTGACAAAGG	SEQ ID NO: 243 GAAGAAATTAGTGTGTTCATCCAATAGAAT		SEQ ID NO: 244
At3g11280	GATGGAGACTCTGCATCCATTCTCACCT	SEQ ID NO: 245 AGCTCCGGCACTGAAGACATTCTCCGGC		SEQ ID NO: 246

TABLE 5-continued

AGI code	Forward primer	Nucleotide sequence	Reverse primer	Nucleotide sequence
At5g07680	GATGGATTTCGCTCCCTGGTTTAG	SEQ ID NO: 247	GTAATTCCAGAAAGGTTCAAGATC	SEQ ID NO: 248
At1g25470	ATGTCGGCTGTGTCATGAATCG	SEQ ID NO: 249	AACCAAACCGAGAGGGCGGTG	SEQ ID NO: 250
At1g28520	GATGACGGGGAAAGCGATCAAAGAC	SEQ ID NO: 251	GGGGATATAATAGTCGCTTAGATTTC	SEQ ID NO: 252
At1g77450	GATGATGAAATCTGGGCTGATTGC	SEQ ID NO: 253	GAAAGTTCCTGCCTAACACAAAGTGG	SEQ ID NO: 254
At5g24590	GATGAAAAGAACATGGAAGTACTATC	SEQ ID NO: 255	TGCGACTAGACTGCAGACCGACATC	SEQ ID NO: 256
At5g08790	GATGAAGTCGGAGCTAAATTACCAAGCTGG	SEQ ID NO: 257	COCTGTGGAGCAAACATCCAATTCAAGAA	SEQ ID NO: 258
At1g67260	ATGTCGTCTTCACCAATGAC	SEQ ID NO: 259	GTTCACAAAAGAGTCTTGAATCC	SEQ ID NO: 260
At4g28530	GATGGGTTGAAAGATATTGGGTCC	SEQ ID NO: 261	TTGGAAAGCGAGGATATTCGCGTC	SEQ ID NO: 262
At5g13910	ATGAACACAAACATCATCAAAGAGC	SEQ ID NO: 263	GGAGGCCAAAGTAGTGTGAAACCTTG	SEQ ID NO: 264
At5g64530	GATGAATCTACCACCGGGATTTAGG	SEQ ID NO: 265	CGGTAAAGCTTACTTCGTCAGATC	SEQ ID NO: 266
At2g33710	ATGCATAGCGGGAAAGAGACCTC	SEQ ID NO: 267	TTTCGTCGTTGTGGATACTAATG	SEQ ID NO: 268
At1g53230	GATGAAGAGAGATCATCATCATCATCA	SEQ ID NO: 269	ATGGCGAGAATCGGATGAAAGC	SEQ ID NO: 270
At1g56010	GATGGAGACGGAAAGAGAGATGAAG	SEQ ID NO: 271	GCAATTCCAAACAGTGCCTGGAAATAC	SEQ ID NO: 272
At5g18560	ATGGGTTTGCTCTGATCCACC	SEQ ID NO: 273	AAAGACTGAGTAGAAGCCTGTAG	SEQ ID NO: 274
At5g67580	GATGGGTGCACCAAAGCAGAAGTGGACACC	SEQ ID NO: 275	CCAAGGATGATTACGGATCCTGAACTTCAA	SEQ ID NO: 276
At5g24520	GATGGATAATTCAAGCTCCAGATTCGTTATC	SEQ ID NO: 277	AACTCTAAGGAGCTGCATTTGTTAGCAA	SEQ ID NO: 278
At4g18390	ATGATTGGAGATCTAATGAAG	SEQ ID NO: 279	GAGACTGATAACCGACACG	SEQ ID NO: 280
At1g69690	GATGAAGAGAGATCATCATCATCATCA	SEQ ID NO: 281	TCAGGAATGATGACTGGTGTCTCC	SEQ ID NO: 282
At5g13330	ATGGTCTCGCTCTCAGCCG	SEQ ID NO: 283	TTATTCTTGGGTAGTTATAATAATTG	SEQ ID NO: 284
At5g60970	ATGAGATCAGGAGAATGTGATG	SEQ ID NO: 285	AGAATCTGATTCTATTACGCTAC	SEQ ID NO: 286
At3g23220	GGGGATGTACGGACAGTGCATATAG	SEQ ID NO: 287	GGGTATGAAACCAATACTCATCACACG	SEQ ID NO: 288
At1g62700	GATGAATTCTGGTTTACAAGTACCTCTGG	SEQ ID NO: 289	GAGATCAATCTGACAACATTGAAGAAGTAGA	SEQ ID NO: 290
At5g13330	ATGGTCTCGCTCTCAGCCG	SEQ ID NO: 291	TTCTCTTGGGTAGTTATAATAATTG	SEQ ID NO: 292
At1g22985	ATGAAACGAATTGTCGAATTCATTC	SEQ ID NO: 293	AAACAATTCTTCAGAAGCACCAC	SEQ ID NO: 294
At5g09330	GATGGGGAAACCTCAACTCGCTCTGGATT	SEQ ID NO: 295	CATTTTGGTCTATGTCTCATGGAAGCAGA	SEQ ID NO: 296
At1g10200	GGGATGGCGTTCGCAGGAACAACCCAGAAA	SEQ ID NO: 297	AGCAGCGACGACTTGTCTTGGCG	SEQ ID NO: 298
	TG			
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At1g30210	ATGGAGGTTGACGAAGACATTG	SEQ ID NO: 301	TCTCCTTCTTGGCTTGTC	SEQ ID NO: 302
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	TAG			
At5g13180	GATGGATAATGTCAAACCTGTTAAGAATGG	SEQ ID NO: 305	TCTGAAACTATTGCAACTACTGGCTCTTC	SEQ ID NO: 306
At1g52880	GATGGAGAGTACAGATTCTCCGGTGGTCC	SEQ ID NO: 307	AGAATACCAATTCAAACCCAGGCAATTGGTA	SEQ ID NO: 308
At4g18450	ATGGCTTGGCAATATCCAAG	SEQ ID NO: 309	AAAAGAAGATAATAACGCTCC	SEQ ID NO: 310
At5g07580	ATGGCGAGTTTGAGGAAAGC	SEQ ID NO: 311	AAATGCATCACAGGAAGATGAAG	SEQ ID NO: 312
At1g74930	ATGGTGAAGCAAGCGATGAAGG	SEQ ID NO: 313	AAAATCCCAAAGAATCAAAGATTC	SEQ ID NO: 314
At4g36160	GATGGAATCGGTGGATCAATCATGTAGTGT	SEQ ID NO: 315	AACATGTAATCCCTATATAAGTCATAGTC	SEQ ID NO: 316
At3g18550	ATGAACAACAAACATTTCACTACTAC	SEQ ID NO: 317	ACTGTGTATAGCTTAGATAAAACC	SEQ ID NO: 318
At5g64750	ATGTGTGCTTAAAGTGGCAAATC	SEQ ID NO: 319	GGAGGATGGACTATTATTGTAG	SEQ ID NO: 320
At2g02450	GATGGCGCGATAGGAGAGAAAAG	SEQ ID NO: 321	CTTAAAAGGAATATTAGTATAGTG	SEQ ID NO: 322

TABLE 5-continued

AGI code	Forward primer	Nucleotide sequence	Reverse primer	Nucleotide sequence
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At5g67300	GATGGCTGATAGGATCAAAGGCCATGGAG	SEQ ID NO: 325 CTCGATTCTCCAACTCCAATTGACTCAT		SEQ ID NO: 326
At1g68800	ATGTTCTTCTTCATTACTCAC	SEQ ID NO: 327 ATTAGGGTTTTAGTTAACACATTG		SEQ ID NO: 328
At1g14510	ATGGAAGGAATTCAAGCATCC	SEQ ID NO: 329 GGCTTCATTTCTGCTGG		SEQ ID NO: 330
At1g25580	GATGGCTGGCGATCATGGCTGATC	SEQ ID NO: 331 CAGCAGCGTGGCAGTGTGTTGCC		SEQ ID NO: 332
At5g18270	GATGGCGGTTGTTGAAGAAGG	SEQ ID NO: 333 GAAGTCCCACAAGTCCCCCTC		SEQ ID NO: 334
At2g44840	ATGAGCTCATCTGATTCCGTTAAC	SEQ ID NO: 335 TATCCGATTATCAGAATAAGAACATT		SEQ ID NO: 336
At3g15500	GATGGGCTCCAAGAGCTTGACCCGTTAGC	SEQ ID NO: 337 AATAAACCGAACCCACTAGATTGTTGACC		SEQ ID NO: 338
At4g35580	GATGCTGCAGTCAGCAGCACAGAG	SEQ ID NO: 339 TGAACTCACCAGTGTCCCTCATATAC		SEQ ID NO: 340
At4g01550	GATGGTGAAGAGATCTGGTTGGG	SEQ ID NO: 341 TCTCTCGCGATCAAACCTCATCGC		SEQ ID NO: 342
At4g37750	ATGAAGTCTTTGTGATAATGATG	SEQ ID NO: 343 AGAACATGCCAACGAGCGAAAACCGG		SEQ ID NO: 344
At1g52890	GATGGGTATCCAAGAAACTGACCCGTTAAC	SEQ ID NO: 345 CATAAACCCAAACCCACCAACTTGCCCCGA		SEQ ID NO: 346
At2g17040	GATGGTTACGGTAAGAGATCGAG	SEQ ID NO: 347 CCAATATATGTTAACATTGGTG		SEQ ID NO: 348
At2g33480	GATGGAGAACAGGGAGCTATTAAAAACAG	SEQ ID NO: 349 TAGAAACAAACAAACTTATTCCCAGATA		SEQ ID NO: 350
At5g39610	GATGGATTACGGAGCATCAAGAACATC	SEQ ID NO: 351 GAAATTCCAAACGCAATCCAATTC		SEQ ID NO: 352
At1g32770	GATGGCTGATAATAAGGTCAATTTCGAT	SEQ ID NO: 353 TACAGATAATGAAGAAGTGGGTCTAAAGA		SEQ ID NO: 354
At5g47220	GAIGTACGGACAGTGCAATATAGAACATCCG	SEQ ID NO: 355 TGAAACCAATAACTCATCAACACGTGT		SEQ ID NO: 356
At1g56650	GGGATGGAGGGTCGCAAAGGGCTUGCGAACAGG	SEQ ID NO: 357 ATCAAATTCACAGTCTCTCCATCGAAAAGACTCC		SEQ ID NO: 358
At1g63910	GATGGGTCATCACTCATGCTGCAACCAGCA	SEQ ID NO: 359 AAACGAAGAAGGGAAAGAAGAAGATAAGGC		SEQ ID NO: 360
At3g15510	GATGGAGAGCACCGATTCTCCGGTGGTCC	SEQ ID NO: 361 AGAAAGAGTACCAATTAAACCGGGTAATTG		SEQ ID NO: 362
At2g45680	ATGGCGACAATTCAAGAGCTTG	SEQ ID NO: 363 GTGGTTCGATGACCGTGCTG		SEQ ID NO: 364
At2g31230	ATGTATTCACTCCAAGTTCTGG	SEQ ID NO: 365 ACATGAGCTCATAGAAAGTTGTT		SEQ ID NO: 366
At1g12260	GATGAATTCAATTCCCACGTCCCTCCGGG	SEQ ID NO: 367 CTTCCATAGATCAATCTGACAACCTCGAAGA		SEQ ID NO: 368
At3g61910	GATGAACATATCAGTAACGGACAGTCACA	SEQ ID NO: 369 TCCACTACCGTTCAACAAAGTGGCATGTCGT		SEQ ID NO: 370
At5g07310	ATGGCGAATTCAAGGAAATTATGG	SEQ ID NO: 371 AAAACCAGAATTAGGAGGTGAAG		SEQ ID NO: 372
At3g14230	ATGTGTGGAGGGCTATAATCTC	SEQ ID NO: 373 AAAGTCTCCTCCAGCATGAAATTG		SEQ ID NO: 374
At1g28160	ATGGAGTTCAATGGTAATTGAATG	SEQ ID NO: 375 TTGGTAGAAGAATGTGGAGGG		SEQ ID NO: 376
At1g69120	GATGGGAAGGGTAGGGTCAATTGAAGAG	SEQ ID NO: 377 TGCGCGAACGAGCCAAGGTTGCAGTTGTA		SEQ ID NO: 378
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At3g15210	GGGGATGGCCAAGATGGCTGAAAC	SEQ ID NO: 385 TCAGGCCTGTTCCGATGGAGGAGC		SEQ ID NO: 386
At4g08150	ATGGAAGAACATCCAGCATGACAAC	SEQ ID NO: 387 TCATGGACCGAGACGATAAGGTCC		SEQ ID NO: 388
At1g10200	GGGATGGCGTCCGAGGAACAACCCAGAAA	SEQ ID NO: 389 TTAAGCAGCGACGACTTGTGCC		SEQ ID NO: 390
	TG			

Production of Improved Transcription Factors

In order to add a repressor domain sequence to the 3' terminal of a transcription factor gene encoded by a coding region DNA fragment excluding a termination codon, p35SSXG, which is a vector having an SmaI site and a repressor domain sequence (amino acid sequence: GLLDLDELR-LGFA (SEQ ID NO: 391) downstream of a CaMV35S promoter, was used. In order to link a transcription factor gene sequence and a repressor domain sequence, p35SSXG was cleaved with SmaI. Each PCR amplification fragment encoding the relevant transcription factor obtained above was separately inserted at the cleavage site. Thus, vectors (each denoted by p35SSXG(TFs)) were produced. Here, each vector is denoted by p35SSXG(TFs), provided that "TFs" represents the AGI code for each transcription factor. For example, a vector having the transcription factor specified by At2g23760 is denoted by p35SSXG(At2g23760). Also, in the descriptions below, "TFs" is used in a similar manner to denote vectors and the like.

Construction of Improved Transcription Factor Expression Vectors

pBCKH was used as a binary vector for gene introduction into plants with *Agrobacterium*. This vector was obtained by incorporating a cassette of the Gateway vector conversion system (Invitrogen) into the HindIII site of pBIG(Hygr) (Nucleic Acids Res. 18,203 (1990)). In order to incorporate an improved transcription factor gene sequence into the vector, 181 types of p35SSXG(TFs) were each separately mixed with the vector, followed by a recombination reaction using GATEWAY LR clonase (Invitrogen). Thus, vectors (each denoted by pBCKH-p35SSXG(TFs)) were produced.

In addition, for each transcription factor encoded by the relevant coding region DNA fragment including a termination codon, the gene encoding the transcription factor was selected for introduction. Thus, vectors, in each of which the relevant DNA fragment was linked downstream of a 35S promoter in the manner described above, were produced.

Introduction of Improved Transcription Factor Gene Expression Vectors and Transcription Factor Expression Vectors into Plants

Arabidopsis thaliana (Columbia (Col-0)) was used as a plant for introduction of a transcription factor or an improved transcription factor. Gene introduction was carried out in accordance with "Transformation of *Arabidopsis thaliana* by vacuum infiltration" (www.bch.msu.edu/pamgreen/protocol.htm). Note that each plant was infected only by immersing it in an *Agrobacterium* bacterial liquid without conducting depressurization treatment. Specifically, a transcription factor expression vector or an improved transcription factor expression vector (pBCKH-p35SSXG(TFs)) was introduced into the soil bacterium (*Agrobacterium tumefaciens*) strain (GV3101 (C58C1Rifr) pMP90 (Gmr), Koncz and Schell 1986)) by electroporation. For each vector, gene-transfected bacterial cells were cultured in 1 liter of a YEP medium containing antibiotics (kanamycin (Km): 50 µg/ml; gentamicin (Gm): 25 µg/ml; and rifampicin (Rif): 50 µg/ml) until OD600 became 1. Subsequently, bacterial cells were recovered from each culture solution and suspended in 1 liter of an infection medium (an infiltration medium containing 2.2 g of an MS salt, 1X B5 vitamins, 50 g of sucrose, 0.5 g of MES, 0.044 µM of benzylaminopurine, and 400µl of Silwet per litter (pH 5.7)).

Arabidopsis thaliana plants cultivated for 14 days were immersed in each solution for 1 minute for infection. Thereafter, the plants were continuously cultivated to result in seed setting. The collected seeds (T1 seeds) were sterilized in a solution containing 50% bleach and 0.02% Triton X-100 for

7 minutes, rinsed 3 times with sterilized water, and seeded on a sterilized hygromycin selection medium (containing a 4.3 g/l MS salt, 0.5% sucrose, 0.5 g/l MES (pH 5.7), 0.8% agar, 30 mg/l hygromycin, and 250 mg/l vancomycin). Five to ten lines of the transformed plants (T1 plants) growing on the hygromycin plate were selected for each improved transcription gene and transplanted into pots (each with a diameter of 50 mm) containing vermiculite mixed soil. Then, the plants were cultivated under conditions of 22° C. for 16 hours in the light and 8 hours in the dark at a light intensity ranging from about 60 to 80 µE/cm². Thus, seeds (T2 seeds) were obtained.

Analysis of T2 Seeds

Forty seeds were weighed and put into a 1.5-ml PP microtest tube for each of the transformants and wild-type *Arabidopsis thaliana*, which had been transfected with the relevant improved transcription factor or transcription factor. Further, a Tungsten Carbide Bead (3 mm) (QIAGEN) was put into each tube, followed by disruption by shaking at a frequency of 1/30 for 1 minute using a Mixer Mill MM 300 (Qiagen). After disruption, 50 µl of extraction buffer (62.5 mM Tris-HCl, 2% SDS, 10% glycerol, and 5% 2-mercaptoethanol) was added thereto, followed by another instance of disruption by shaking for 1 minute. After disruption, each tube was allowed to stand on ice for 10 minutes, followed by centrifugation at 15000 rpm for 10 minutes. Each obtained supernatant was subjected to quantitative protein determination.

Quantitative protein determination for the prepared extracts was carried out using RC DC Protein Assay Kits (Bio-Rad) according to the manufacturer's instructions. The protein concentration was determined based on a calibration curve derived from BSA (bovine serum albumin).

In addition, 34 individuals of the wild strain (Col-0) were cultivated and seeds were collected from each individual. The protein content was determined for each line by quantitative analysis. Then, the average protein content was obtained. Thereafter, the average protein content of each transgenic individual was compared with the average protein content of the wild strain. The protein content increase rate for each gene-transfected line and the t-test P value were determined. Each line was found to exhibit improvement or reduction of seed protein content by 20% or more when compared with a wild-type strain. However, the P value was found to be 5% or less for each comparison.

Table 6 lists the analysis results for each line that was found to exhibit improvement of seed protein content by 20% or more as a result of introduction of the relevant improved transcription factor when compared with the wild-type strain. Table 7 lists the analysis results for each line that were found to exhibit improvement of seed protein content by 20% or more as a result of introduction of the gene encoding the relevant transcription factor when compared with the wild-type strain.

TABLE 6

AGI code	Reference number	Protein content (%)	Increase-decrease rate (%)
	WT(Col-0)	16.3%	—
1	At2g23760	25.7%	57.5%
2	At1g18330	25.2%	54.2%
3	At2g02070	23.9%	46.3%
4	At1g12980	22.6%	38.7%
5	At5g62380	22.5%	38.2%
6	At4g23750	21.8%	33.7%
7	At4g32800	21.6%	32.1%

TABLE 6-continued

AGI code	Reference number	Protein content (%)	Increase-decrease rate (%)
8	At1g24590	CR019	21.4%
9	At5g07690	HR0040	21.2%
10	At1g71692	CR412	21.0%
11	At1g52150	HR0611	20.9%
12	At3g25890	CR029	20.4%
13	At1g09540	CR705	20.4%
14	At5g22380	CR229	20.3%
15	At2g44940	CR505	20.3%
16	At5g41030	CR131	20.2%
17	At5g60970	CR116	20.1%
18	At5g35550	CR701	20.0%
19	At1g60240	CR623	19.9%
20	At2g23290	HR0018	19.9%
21	At5g14000	CR223	19.7%
22	At1g19490	HR0001	19.6%

TABLE 7

AGI code	Reference number	Protein content (%)	Increase-decrease rate (%)
	WT(Col-0)	16.3%	—
1	At3g04070	CR312	22.1%
2	At2g46770	CR308	21.0%
3	At5g35550	CR903	21.0%

Table 8 lists the analysis results for each line that was found to exhibit reduction of seed protein content by 20% or more as a result of introduction of the relevant improved transcription factor when compared with the wild-type strain. Table 9 lists the analysis results for each line that were found to exhibit reduction of seed protein content by 20% or more as a result of introduction of the gene encoding the relevant transcription factor when compared with a wild-type strain.

TABLE 8

AGI code	Reference number	Protein content (%)	Increase-decrease rate (%)
	WT(Col-0)	16.3%	0.0%
1	At1g32770	CR250	12.8%
2	At5g47220	TP100	12.8%
3	At1g56650	TP107	12.7%
4	At1g63910	HR1722	12.5%
5	At3g15510	CR245	12.5%
6	At2g45680	CR121	12.4%
7	At2g31230	CR006	12.2%
8	At1g12260	CR232	12.1%
9	At3g61910	CR601	11.9%
10	At5g07310	CR008	11.9%
11	At3g14230	CR014	11.9%
12	At1g28160	CR020	11.8%
13	At1g69120	CR404	11.8%
14	At3g10490	CR220	11.8%
15	At5g61600	CR001	11.5%
16	At1g43160	CR015	10.9%

TABLE 9

AGI code	Reference number	Protein content (%)	Increase-decrease rate (%)
	WT(Col-0)	16.3%	0.0%
1	At1g10200	TP106	13.0%

In addition, T2 seeds of a line (HR0530) (into which the improved transcription factor (At2g23760) listed in FIG. 6 with the results demonstrating the largest increase in protein content had been introduced) were cultivated, followed by re-evaluation of the protein content. Table 10 lists the results. As shown in table 10, it was also possible to confirm an increase in protein content for T3 seeds. In particular, the protein content was found to be up to 43% higher than that of the wild-type line. In addition, it was confirmed that SDS-PAGE caused no changes in seed protein composition (not shown).

TABLE 10

	In-Protein concentration (mg/ml)	increasing rate (%)	In-Protein content (%)	Increasing rate (%)	Total protein amount (mg)	Increasing rate (%)
Average of WT (10 individuals)	1.6	—	26.6	—	71.8	—
HR0530-23-4	2.4	46.3	36.9	38.5	90.7	26.3
HR0530-23-10	2.3	43.0	39.4	48.2	130.1	81.1
HR0530-23-8	2.3	39.6	39.0	46.7	103.9	44.7

As described above, the expression of SRDX-added chimeric proteins formed with 141 types of transcription factors was induced in this analysis. Results showed that the seed storage protein content increased by 20% or more as a result of expression of 22 types of chimeric proteins (accounting for 15.6% of the analyzed transcription factors), while the seed storage protein content decreased by 20% or more as a result of expression of 16 types of chimeric proteins (accounting for 11.3% of the analyzed transcription factors). That is to say, the seed storage protein content was found to have remarkably increased or decreased as a result of expression of approximately 27% of the chimeric proteins. In other words, it was found that approximately 73% of the transcription factors (e.g., At3g23220, At1g18570, At3g01530, At5g51190, At4g34410, At5g22290, and At3g04420) subjected to the experiments in the Examples do not cause remarkable changes in seed protein content even when a chimeric protein comprising such a transcription factor and a repressor domain is expressed or such a transcription factor is overexpressed.

As described above, the Examples revealed that the seed protein content can be significantly modified by causing expression of a particular transcription factor fused with a repressor domain, introducing a gene encoding a particular transcription factor, or modifying an expression control region of such gene.

In addition, in order to increase or decrease the seed protein content with the use of the above functionally improved transcription factors, it is expected that it will become possible to further modify the storage protein content to a remarkable extent with the simultaneous use of transcription factors and a known method for modifying a seed storage protein by modifying the nitrogen metabolic pathway, the fatty acid metabolic pathway, or transcription factors.

All publications, patents, and patent applications cited herein are incorporated herein by reference in their entirety.

SEQUENCE LISTING

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Phe Thr Asp Glu Asn Thr Met Gln Pro Gln Gln Gln His Phe Thr
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Trp Pro Ser Ser Ser Ser Asp His His Gln Asn Arg Asp Met Ile Gly
 130 135 140

Thr Val His Val Glu Gly Gly Lys Gly Leu Ser Leu Ser Leu Ser Ser
 145 150 155 160

Ser Leu Ala Ala Ala Lys Ala Glu Glu Tyr Arg Ser Ile Tyr Cys Ala
 165 170 175

Ala Val Asp Gly Thr Ser Ser Ser Asn Ala Ser Ala His His His
 180 185 190

Gln Phe Asn Gln Phe Lys Asn Leu Leu Leu Glu Asn Ser Ser Ser Gln
 195 200 205

His His His His Gln Val Val Gly His Phe Gly Ser Ser Ser Ser Ser
 210 215 220

Pro Met Ala Ala Ser Ser Ser Ile Gly Gly Ile Tyr Thr Leu Arg Asn
 225 230 235 240

Ser Lys Tyr Thr Lys Pro Ala Gln Glu Leu Leu Glu Glu Phe Cys Ser
 245 250 255

Val Gly Arg Gly His Phe Lys Lys Asn Lys Leu Ser Arg Asn Asn Ser
 260 265 270

Asn Pro Asn Thr Thr Gly Gly Gly Gly Ser Ser Ser Ser
 275 280 285

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35**36**

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Ala Gly Thr Ala Asn Asp Ser Pro Pro Leu Ser Pro Ala Asp Arg Ile
 290 295 300
 Glu His Gln Arg Arg Lys Val Lys Leu Leu Ser Met Leu Glu Glu Val
 305 310 315 320
 Asp Arg Arg Tyr Asn His Tyr Cys Glu Gln Met Gln Met Val Val Asn
 325 330 335
 Ser Phe Asp Gln Val Met Gly Tyr Gly Ala Ala Val Pro Tyr Thr Thr
 340 345 350
 Leu Ala Gln Lys Ala Met Ser Arg His Phe Arg Cys Leu Lys Asp Ala
 355 360 365
 Val Ala Val Gln Leu Lys Arg Ser Cys Glu Leu Leu Gly Asp Lys Glu
 370 375 380
 Ala Ala Gly Ala Ala Ser Ser Gly Leu Thr Lys Gly Glu Thr Pro Arg
 385 390 395 400
 Leu Arg Leu Leu Glu Gln Ser Leu Arg Gln Gln Arg Ala Phe His His
 405 410 415
 Met Gly Met Met Glu Gln Glu Ala Trp Arg Pro Gln Arg Gly Leu Pro
 420 425 430
 Glu Arg Ser Val Asn Ile Leu Arg Ala Trp Leu Phe Glu His Phe Leu
 435 440 445
 Asn Pro Tyr Pro Ser Asp Ala Asp Lys His Leu Leu Ala Arg Gln Thr
 450 455 460
 Gly Leu Ser Arg Asn Gln Val Ser Asn Trp Phe Ile Asn Ala Arg Val
 465 470 475 480
 Arg Leu Trp Lys Pro Met Val Glu Glu Met Tyr Gln Gln Glu Ala Lys
 485 490 495
 Glu Arg Glu Glu Ala Glu Glu Asn Glu Asn Gln Gln Gln Arg
 500 505 510
 Arg Gln Gln Gln Thr Asn Asn Asn Asp Thr Lys Pro Asn Asn Asn Glu
 515 520 525
 Asn Asn Phe Thr Val Ile Thr Ala Gln Thr Pro Thr Thr Met Thr Ser
 530 535 540
 Thr His His Glu Asn Asp Ser Ser Phe Leu Ser Ser Val Ala Ala Ala
 545 550 555 560
 Ser His Gly Gly Ser Asp Ala Phe Thr Val Ala Thr Cys Gln Gln Asp
 565 570 575
 Val Ser Asp Phe His Val Asp Gly Asp Gly Val Asn Val Ile Arg Phe
 580 585 590
 Gly Thr Lys Gln Thr Gly Asp Val Ser Leu Thr Leu Gly Leu Arg His
 595 600 605
 Ser Gly Asn Ile Pro Asp Lys Asn Thr Ser Phe Ser Val Arg Asp Phe
 610 615 620
 Gly Asp Phe
 625

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<210> SEQ_ID NO 3
<211> LENGTH: 1119
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1119)
  
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<400> SEQUENCE: 3

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atg ctc tgt ttt gtt cgc ttt cag gct ggt ttt gtg aga att ata gtt Met Leu Cys Phe Val Arg Phe Gln Ala Gly Phe Val Arg Ile Ile Val 1 5 10 15	48
gca gca aga aag cgt ttc aga tat ttt tta atg gcc gct gag gat cga Ala Ala Arg Lys Arg Phe Arg Tyr Phe Leu Met Ala Ala Glu Asp Arg 20 25 30	96
agt gag gaa cta agc agc aat gta gaa aat gga agt tgc aat tcc aat Ser Glu Glu Leu Ser Ser Asn Val Glu Asn Gly Ser Cys Asn Ser Asn 35 40 45	144
gaa gga att aat cct gaa acc agc agt cat tgg att gaa aac gtt gtc Glu Gly Ile Asn Pro Glu Thr Ser Ser His Trp Ile Glu Asn Val Val 50 55 60	192
aag gtt agg aaa ccg tac aca gta act aag cag aga gag aag tgg agt Lys Val Arg Lys Pro Tyr Thr Val Thr Lys Gln Arg Glu Lys Trp Ser 65 70 75 80	240
gag gaa gag cat gat agg ttt ctt gaa gct atc aag ctt tat ggt cgt Glu Glu His Asp Arg Phe Leu Glu Ala Ile Lys Leu Tyr Gly Arg 85 90 95	288
ggt tgg cgt caa atc caa gaa cac ata ggt aca aaa acc gct gta cag Gly Trp Arg Gln Ile Gln Glu His Ile Gly Thr Lys Thr Ala Val Gln 100 105 110	336
ata cga agc cat gct caa aag ttc ttc tcc aag atg gct cag gaa gct Ile Arg Ser His Ala Gln Lys Phe Phe Ser Lys Met Ala Gln Glu Ala 115 120 125	384
gac agt aga agt gaa gga tcg gtt aaa gcg att gtg atc ccg cct cct Asp Ser Arg Ser Glu Gly Ser Val Lys Ala Ile Val Ile Pro Pro Pro 130 135 140	432
cgt cca aag aga aaa ccg gca cat cct tat cct ccg aaa tcg cct gtt Arg Pro Lys Arg Lys Pro Ala His Pro Tyr Pro Arg Lys Ser Pro Val 145 150 155 160	480
cca tat act cag tct cct cca cca aat ttg tca gct atg gag aaa gga Pro Tyr Thr Gln Ser Pro Pro Asn Leu Ser Ala Met Glu Lys Gly 165 170 175	528
acc aag tct cca acc tca gtg tta tca tcg ttt ggt tca gag gat caa Thr Lys Ser Pro Thr Ser Val Leu Ser Ser Phe Gly Ser Glu Asp Gln 180 185 190	576
gtc aat aga tgc tct tcg cct aat tcg tgt acc agt gac atc caa tcc Val Asn Arg Cys Ser Ser Pro Asn Ser Cys Thr Ser Asp Ile Gln Ser 195 200 205	624
att ggt gca act tcc att gat aaa aag aat aac tac aca aca tcc aag Ile Gly Ala Thr Ser Ile Asp Lys Lys Asn Asn Tyr Thr Thr Ser Lys 210 215 220	672
caa cct ttc aaa gat gat tct gac att ggt tca aca ccc att tca agc Gln Pro Phe Lys Asp Asp Ser Asp Ile Gly Ser Thr Pro Ile Ser Ser 225 230 235 240	720
att act ctt ttc ggg aag att gtc ctt gtc gcg gaa gaa tct cac aaa Ile Thr Leu Phe Gly Lys Ile Val Leu Val Ala Glu Glu Ser His Lys 245 250 255	768
cca tcc tct tac aat gat gat gat ctt aaa caa atg acg tgt cag gag Pro Ser Ser Tyr Asn Asp Asp Asp Leu Lys Gln Met Thr Cys Gln Glu 260 265 270	816
aat cac tac tca ggg atg cta gtt gac act aat tta tct ctt ggt gta Asn His Tyr Ser Gly Met Leu Val Asp Thr Asn Leu Ser Leu Gly Val 275 280 285	864
tgg gaa acg ttt tgt act ggt tct aat gca ttt ggc tcg gtt aca gaa Trp Glu Thr Phe Cys Thr Gly Ser Asn Ala Phe Gly Ser Val Thr Glu 290 295 300	912
gca tct gag aac ttg gag aaa agt gca gag ccg ata agt tct tca tgg Ala Ser Glu Asn Leu Glu Lys Ser Ala Glu Pro Ile Ser Ser Ser Trp 305 310 315 320	960

aaa cggtta agctcc tta gaa aaa caa gga tct tgt aat cct gta aat
 Lys Arg Leu Ser Ser Leu Glu Lys Gln Gly Ser Cys Asn Pro Val Asn
 325 330 335

gca agt ggg ttccaggcca tac aag aga tgc cta tca gaa aga gaa gta
 Ala Ser Gly Phe Arg Pro Tyr Lys Arg Cys Leu Ser Glu Arg Glu Val
 340 345 350

aca tca tca ttg acgtcg gta gct tca gat gaa aag aaa agc caa aga
 Thr Ser Ser Leu Thr Leu Val Ala Ser Asp Glu Lys Lys Ser Gln Arg
 355 360 365

gca cgt ata tgc tag
 Ala Arg Ile Cys
 370

<210> SEQ ID NO 4
<211> LENGTH: 372
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 4

Met Leu Cys Phe Val Arg Phe Gln Ala Gly Phe Val Arg Ile Ile Val
 1 5 10 15

Ala Ala Arg Lys Arg Phe Arg Tyr Phe Leu Met Ala Ala Glu Asp Arg
 20 25 30

Ser Glu Glu Leu Ser Ser Asn Val Glu Asn Gly Ser Cys Asn Ser Asn
 35 40 45

Glu Gly Ile Asn Pro Glu Thr Ser Ser His Trp Ile Glu Asn Val Val
 50 55 60

Lys Val Arg Lys Pro Tyr Thr Val Thr Lys Gln Arg Glu Lys Trp Ser
 65 70 75 80

Glu Glu Glu His Asp Arg Phe Leu Glu Ala Ile Lys Leu Tyr Gly Arg
 85 90 95

Gly Trp Arg Gln Ile Gln Glu His Ile Gly Thr Lys Thr Ala Val Gln
 100 105 110

Ile Arg Ser His Ala Gln Lys Phe Phe Ser Lys Met Ala Gln Glu Ala
 115 120 125

Asp Ser Arg Ser Glu Gly Ser Val Lys Ala Ile Val Ile Pro Pro Pro
 130 135 140

Arg Pro Lys Arg Lys Pro Ala His Pro Tyr Pro Arg Lys Ser Pro Val
 145 150 155 160

Pro Tyr Thr Gln Ser Pro Pro Asn Leu Ser Ala Met Glu Lys Gly
 165 170 175

Thr Lys Ser Pro Thr Ser Val Leu Ser Ser Phe Gly Ser Glu Asp Gln
 180 185 190

Val Asn Arg Cys Ser Ser Pro Asn Ser Cys Thr Ser Asp Ile Gln Ser
 195 200 205

Ile Gly Ala Thr Ser Ile Asp Lys Lys Asn Asn Tyr Thr Thr Ser Lys
 210 215 220

Gln Pro Phe Lys Asp Asp Ser Asp Ile Gly Ser Thr Pro Ile Ser Ser
 225 230 235 240

Ile Thr Leu Phe Gly Lys Ile Val Leu Ala Glu Glu Ser His Lys
 245 250 255

Pro Ser Ser Tyr Asn Asp Asp Asp Leu Lys Gln Met Thr Cys Gln Glu
 260 265 270

Asn His Tyr Ser Gly Met Leu Val Asp Thr Asn Leu Ser Leu Gly Val
 275 280 285

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Trp Glu Thr Phe Cys Thr Gly Ser Asn Ala Phe Gly Ser Val Thr Glu
290 295 300

Ala Ser Glu Asn Leu Glu Lys Ser Ala Glu Pro Ile Ser Ser Ser Trp
305 310 315 320

Lys Arg Leu Ser Ser Leu Glu Lys Gln Gly Ser Cys Asn Pro Val Asn
325 330 335

Ala Ser Gly Phe Arg Pro Tyr Lys Arg Cys Leu Ser Glu Arg Glu Val
340 345 350

Thr Ser Ser Leu Thr Leu Val Ala Ser Asp Glu Lys Lys Ser Gln Arg
355 360 365

Ala Arg Ile Cys
370

<210> SEQ_ID NO 5

<211> LENGTH: 1809

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)...(1809)

<400> SEQUENCE: 5

atg gct gtc tct tca tcc tcc gct gtc tcc ttc ttt gga gtc cga caa 48
Met Ala Ala Ser Ser Ser Ala Ala Ser Phe Phe Gly Val Arg Gln
1 5 10 15

gat gac caa tct cac ctc ctc cca cct aat tcc tcc gcc gct gtc cct 96
Asp Asp Gln Ser His Leu Leu Pro Pro Asn Ser Ser Ala Ala Ala Pro
20 25 30

cct cct cca cct cct cac cac cag gca ccg ctg cca ccg ctt gaa gct 144
Pro Pro Pro Pro His His Gln Ala Pro Leu Pro Pro Leu Glu Ala
35 40 45

cca ccg cag aaa aag aag aga aac caa cca aga act cca aat tcc gat 192
Pro Pro Gln Lys Lys Arg Asn Gln Pro Arg Thr Pro Asn Ser Asp
50 55 60

gcg gaa gtg ata gct tta tct cca aag aca cta atg gct aca aac aga 240
Ala Glu Val Ile Ala Leu Ser Pro Lys Thr Leu Met Ala Thr Asn Arg
65 70 75 80

ttc ata tgt gaa gta tgc aac aaa ggg ttt caa aga gaa cag aat cta 288
Phe Ile Cys Glu Val Cys Asn Lys Gly Phe Gln Arg Glu Gln Asn Leu
85 90 95

caa ctt cac cga aga gga cac aat ctt cca tgg aag ctc aaa cag aaa 336
Gln Leu His Arg Arg Gly His Asn Leu Pro Trp Lys Leu Lys Gln Lys
100 105 110

tcg acc aaa gaa gtg aag aga aaa gtg tat ctt tgt ccg gag ccc tcg 384
Ser Thr Lys Glu Val Lys Arg Lys Val Tyr Leu Cys Pro Glu Pro Ser
115 120 125

tgc gtc cac cat gac ccg tca cgt gct ctc gga gac ctc acc gga atc 432
Cys Val His His Asp Pro Ser Arg Ala Leu Gly Asp Leu Thr Gly Ile
130 135 140

aag aaa cat tat tac cgt aaa cac ggt gaa aag aag tgg aaa tgc gat 480
Lys Lys His Tyr Tyr Arg Lys His Gly Glu Lys Lys Trp Lys Cys Asp
145 150 155 160

aaa tgc tct aag cgt tac gct gtt caa tcg gat tgg aaa gct cac tcc 528
Lys Cys Ser Lys Arg Tyr Ala Val Gln Ser Asp Trp Lys Ala His Ser
165 170 175

aag act tgt ggt acc aaa gag tat cgt tgt gac tgt ggt aca ctc ttc 576
Lys Thr Cys Gly Thr Lys Glu Tyr Arg Cys Asp Cys Gly Thr Leu Phe
180 185 190

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tct cgg cga gac agt ttc atc aca cat aga gct ttc tgt gac gcg ttg Ser Arg Arg Asp Ser Phe Ile Thr His Arg Ala Phe Cys Asp Ala Leu 195 200 205	624
gct caa gag agt gcg aga cac cca act tca ttg act tct ttg cca agt Ala Gln Glu Ser Ala Arg His Pro Thr Ser Leu Thr Ser Leu Pro Ser 210 215 220	672
cat cac ttc ccg tac gga caa aac aca aac tcc aac aac gct His His Phe Pro Tyr Gly Gln Asn Thr Asn Ser Asn Asn Asn Ala 225 230 235 240	720
tca agc atg atc ctt ggt ctg tcc cac atg ggg gcc cca cag aat ctt Ser Ser Met Ile Leu Gly Leu Ser His Met Gly Ala Pro Gln Asn Leu 245 250 255	768
gat cac cag ccc ggt gac gtt ctc cgt ctt gga agc gga gga gga Asp His Gln Pro Gly Asp Val Leu Arg Leu Gly Ser Gly Gly Gly 260 265 270	816
gga gga gcc gct tca cgc tct tct gat ctc att gct gcg aat gct Gly Gly Ala Ala Ser Arg Ser Ser Asp Leu Ile Ala Ala Asn Ala 275 280 285	864
tca ggc tac ttc atg caa gag caa aac cct agc ttt cat gat caa caa Ser Gly Tyr Phe Met Gln Glu Gln Asn Pro Ser Phe His Asp Gln Gln 290 295 300	912
gat cat cat cat cat caa caa ggg ttt ttg gct ggg aac aat aac Asp His His His His Gln Gln Gly Phe Leu Ala Gly Asn Asn Asn 305 310 315 320	960
atc aag caa tca cca atg agt ttt caa cag aat ctg atg cag ttc tca Ile Lys Gln Ser Pro Met Ser Phe Gln Gln Asn Leu Met Gln Phe Ser 325 330 335	1008
cat gat aac cat aat tct gct ccc tcc aat gtc ttc aat ctc agc ttc His Asp Asn His Asn Ser Ala Pro Ser Asn Val Phe Asn Leu Ser Phe 340 345 350	1056
ctc tcc gga aac aac gga gtt act tct gcc aca agt aac cct aat gct Leu Ser Gly Asn Asn Gly Val Thr Ser Ala Thr Ser Asn Pro Asn Ala 355 360 365	1104
gcc gcc gct gct gtt tct tct ggt aat ctt atg ata tca aac cat Ala Ala Ala Ala Val Ser Ser Gly Asn Leu Met Ile Ser Asn His 370 375 380	1152
tat gat ggc gaa aat gct gtt gga gga gga gaa gga agc act ggt Tyr Asp Gly Glu Asn Ala Val Gly Gly Glu Gly Ser Thr Gly 385 390 395 400	1200
ctc ttc cct aac aat ctg atg agc tcg gca gat aga att agc tca gga Leu Phe Pro Asn Asn Leu Met Ser Ser Ala Asp Arg Ile Ser Ser Gly 405 410 415	1248
tca gtc cct tca ctc ttt agc tca tca atg caa agt cca aat tca gca Ser Val Pro Ser Leu Phe Ser Ser Met Gln Ser Pro Asn Ser Ala 420 425 430	1296
cct cac atg tca gcc act gcc ctt cta cag aaa gct gct caa atg ggt Pro His Met Ser Ala Thr Ala Leu Leu Gln Lys Ala Ala Gln Met Gly 435 440 445	1344
tca acc tca agc aac aac aac gga agc aac acc aac aac aat aac Ser Thr Ser Asn Asn Asn Gly Ser Asn Thr Asn Asn Asn Asn 450 455 460	1392
aat gcc tca tcg atc cta aga agc ttt ggg agt gga atc tac gga gaa Asn Ala Ser Ser Ile Leu Arg Ser Phe Gly Ser Gly Ile Tyr Gly Glu 465 470 475 480	1440
aat gag agt aat ctt cag gat ttg atg aat tct ttc tct aac ccc ggc Asn Glu Ser Asn Leu Gln Asp Leu Met Asn Ser Phe Ser Asn Pro Gly 485 490 495	1488
gca acg gga aac gtt aac gga gtt gat tct cct ttt ggt tcg tac gga Ala Thr Gly Asn Val Asn Gly Val Asp Ser Pro Phe Gly Ser Tyr Gly 500 505 510	1536

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gga gtg aac aaa gga tta agc gct gac aaa cag agc atg act aga gac Gly Val Asn Lys Gly Leu Ser Ala Asp Lys Gln Ser Met Thr Arg Asp 515 520 525	1584
ttt ctt gga gtt gga cag atc gta aaa agc atg agt gga agc gga ggg Phe Leu Gly Val Gly Gln Ile Val Lys Ser Met Ser Gly Ser Gly Gly 530 535 540	1632
ttt caa caa cag caa caa cag cag caa caa caa caa caa caa Phe Gln Gln 545 550 555 560	1680
cat gga aat agt aga gaa aga gtt ggc tcg tcg tcg gat tcc gct gat His Gly Asn Ser Arg Glu Arg Val Gly Ser Ser Ser Asp Ser Ala Asp 565 570 575	1728
aga agc agc atg aat gtg aat acc gga ggt ggt ccg gca agt act tca Arg Ser Ser Met Asn Val Asn Thr Gly Gly Pro Ala Ser Thr Ser 580 585 590	1776
cca cct tat gga atc cat cat gcg agt ttc taa Pro Pro Tyr Gly Ile His His Ala Ser Phe 595 600	1809

<210> SEQ ID NO 6
<211> LENGTH: 602
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 6

Met Ala Ala Ser Ser Ser Ala Ala Ser Phe Phe Gly Val Arg Gln 1 5 10 15
Asp Asp Gln Ser His Leu Leu Pro Pro Asn Ser Ser Ala Ala Ala Pro 20 25 30
Pro Pro Pro Pro His His Gln Ala Pro Leu Pro Pro Leu Glu Ala 35 40 45
Pro Pro Gln Lys Lys Arg Asn Gln Pro Arg Thr Pro Asn Ser Asp 50 55 60
Ala Glu Val Ile Ala Leu Ser Pro Lys Thr Leu Met Ala Thr Asn Arg 65 70 75 80
Phe Ile Cys Glu Val Cys Asn Lys Gly Phe Gln Arg Glu Gln Asn Leu 85 90 95
Gln Leu His Arg Arg Gly His Asn Leu Pro Trp Lys Leu Lys Gln Lys 100 105 110
Ser Thr Lys Glu Val Lys Arg Lys Val Tyr Leu Cys Pro Glu Pro Ser 115 120 125
Cys Val His His Asp Pro Ser Arg Ala Leu Gly Asp Leu Thr Gly Ile 130 135 140
Lys Lys His Tyr Tyr Arg Lys His Gly Glu Lys Lys Trp Lys Cys Asp 145 150 155 160
Lys Cys Ser Lys Arg Tyr Ala Val Gln Ser Asp Trp Lys Ala His Ser 165 170 175
Lys Thr Cys Gly Thr Lys Glu Tyr Arg Cys Asp Cys Gly Thr Leu Phe 180 185 190
Ser Arg Arg Asp Ser Phe Ile Thr His Arg Ala Phe Cys Asp Ala Leu 195 200 205
Ala Gln Glu Ser Ala Arg His Pro Thr Ser Leu Thr Ser Leu Pro Ser 210 215 220
His His Phe Pro Tyr Gly Gln Asn Thr Asn Asn Ser Asn Asn Ala 225 230 235 240

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Ser Ser Met Ile Leu Gly Leu Ser His Met Gly Ala Pro Gln Asn Leu
245 250 255

Asp His Gln Pro Gly Asp Val Leu Arg Leu Gly Ser Gly Gly Gly
260 265 270

Gly Gly Ala Ala Ser Arg Ser Ser Asp Leu Ile Ala Ala Asn Ala
275 280 285

Ser Gly Tyr Phe Met Gln Glu Gln Asn Pro Ser Phe His Asp Gln Gln
290 295 300

Asp His His His His Gln Gln Gly Phe Leu Ala Gly Asn Asn Asn
305 310 315 320

Ile Lys Gln Ser Pro Met Ser Phe Gln Gln Asn Leu Met Gln Phe Ser
325 330 335

His Asp Asn His Asn Ser Ala Pro Ser Asn Val Phe Asn Leu Ser Phe
340 345 350

Leu Ser Gly Asn Asn Gly Val Thr Ser Ala Thr Ser Asn Pro Asn Ala
355 360 365

Ala Ala Ala Ala Ala Val Ser Ser Gly Asn Leu Met Ile Ser Asn His
370 375 380

Tyr Asp Gly Glu Asn Ala Val Gly Gly Gly Glu Gly Ser Thr Gly
385 390 395 400

Leu Phe Pro Asn Asn Leu Met Ser Ser Ala Asp Arg Ile Ser Ser Gly
405 410 415

Ser Val Pro Ser Leu Phe Ser Ser Ser Met Gln Ser Pro Asn Ser Ala
420 425 430

Pro His Met Ser Ala Thr Ala Leu Leu Gln Lys Ala Ala Gln Met Gly
435 440 445

Ser Thr Ser Ser Asn Asn Asn Gly Ser Asn Thr Asn Asn Asn Asn
450 455 460

Asn Ala Ser Ser Ile Leu Arg Ser Phe Gly Ser Gly Ile Tyr Gly Glu
465 470 475 480

Asn Glu Ser Asn Leu Gln Asp Leu Met Asn Ser Phe Ser Asn Pro Gly
485 490 495

Ala Thr Gly Asn Val Asn Gly Val Asp Ser Pro Phe Gly Ser Tyr Gly
500 505 510

Gly Val Asn Lys Gly Leu Ser Ala Asp Lys Gln Ser Met Thr Arg Asp
515 520 525

Phe Leu Gly Val Gly Gln Ile Val Lys Ser Met Ser Gly Ser Gly Gly
530 535 540

Phe Gln
545 550 555 560

His Gly Asn Ser Arg Glu Arg Val Gly Ser Ser Ser Asp Ser Ala Asp
565 570 575

Arg Ser Ser Met Asn Val Asn Thr Gly Gly Gly Pro Ala Ser Thr Ser
580 585 590

Pro Pro Tyr Gly Ile His His Ala Ser Phe
595 600

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<210> SEQ ID NO 7
<211> LENGTH: 987
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(987)

<400> SEQUENCE: 7

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atg gaa aaa gcc ttg aga aac ttc acc gaa tct acc cac tca cca gac Met Glu Lys Ala Leu Arg Asn Phe Thr Glu Ser Thr His Ser Pro Asp 1 5 10 15	48
cct aat cct ctc aca aaa ttc ttc act gaa cct aca gcc tca cct gtt Pro Asn Pro Leu Thr Lys Phe Phe Thr Glu Pro Thr Ala Ser Pro Val 20 25 30	96
agc cgc aac cgc aaa ctg tct tca aaa gat acc act gta acc atc gcc Ser Arg Asn Arg Lys Leu Ser Ser Lys Asp Thr Thr Val Thr Ile Ala 35 40 45	144
gga gct ggc agc agc acg agg tac cgc ggc gta cgc cgg agg ccc Gly Ala Gly Ser Ser Thr Thr Arg Tyr Arg Gly Val Arg Arg Arg Pro 50 55 60	192
tgg gga cga tac gcg gcg gag ata cgt gac cca atg tcg aag gag aga Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Met Ser Lys Glu Arg 65 70 75 80	240
cgt tgg ctc gga aca ttt gac acg gcg gaa caa gcc gct tgt gct tac Arg Trp Leu Gly Thr Phe Asp Thr Ala Glu Gln Ala Ala Cys Ala Tyr 85 90 95	288
gac tct gcg gct cgt gcc ttt cgt gga gca aag gct cgt act aat ttt Asp Ser Ala Ala Arg Ala Phe Arg Gly Ala Lys Ala Arg Thr Asn Phe 100 105 110	336
act tat ccg aca gct gtc att atg cct gaa cca agg ttt tct ttt tcc Thr Tyr Pro Thr Ala Val Ile Met Pro Glu Pro Arg Phe Ser Phe Ser 115 120 125	384
aac aag aaa tct tcg ccg tct gct cgt ttt ctt cct tct cta ccg Asn Lys Ser Ser Pro Ser Ala Arg Cys Pro Leu Pro Ser Leu Pro 130 135 140	432
tta gat tcc tct acc caa aac ttt tac ggt gca ccg gca gcg cag agg Leu Asp Ser Ser Thr Gln Asn Phe Tyr Gly Ala Pro Ala Ala Gln Arg 145 150 155 160	480
atc tat aat aca cag tct atc ttc tta cgc gac gcc tcg tgt tcc tct Ile Tyr Asn Thr Gln Ser Ile Phe Leu Arg Asp Ala Ser Cys Ser Ser 165 170 175	528
cgt aaa acg act ccg tat aat aac tct ttc aac ggc tca tca tct tct Arg Lys Thr Thr Pro Tyr Asn Asn Ser Phe Asn Gly Ser Ser Ser 180 185 190	576
tac tca gca tcg aaa acg gca tgc gtt tct tat tcc gaa aac gaa aac Tyr Ser Ala Ser Lys Thr Ala Cys Val Ser Tyr Ser Glu Asn Glu Asn 195 200 205	624
aac gag tcg ttt ttc ccg gaa gaa tct tct gat act ggt cta tta caa Asn Glu Ser Phe Phe Pro Glu Glu Ser Ser Asp Thr Gly Leu Leu Gln 210 215 220	672
gag gtc gtt caa gag ttc ttg aag aaa aat cgc ggc gtt cct cct tct Glu Val Val Gln Glu Phe Leu Lys Lys Asn Arg Gly Val Pro Pro Ser 225 230 235 240	720
cca cca aca cca ccg ccg gtg act agc cat cat gac aac tct ggt tat Pro Pro Thr Pro Pro Val Thr Ser His His Asp Asn Ser Gly Tyr 245 250 255	768
ttc tct aat ctc act ata tac tct gaa aat atg gtt caa gag act aag Phe Ser Asn Leu Thr Ile Tyr Ser Glu Asn Met Val Gln Glu Thr Lys 260 265 270	816
gag act ttg tcg tcg aaa cta gat cgc tac ggg aat ttt caa gct aat Glu Thr Leu Ser Ser Lys Leu Asp Arg Tyr Gly Asn Phe Gln Ala Asn 275 280 285	864
gac gac ggc gta aga gcc gtc gca gac ggt ggt tta tcg ttg gga tca Asp Asp Gly Val Arg Ala Val Ala Asp Gly Gly Leu Ser Leu Gly Ser 290 295 300	912

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51**52**

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aac gag tgg ggg tat caa gaa atg ttg atg tac gga act cag tta ggc	960
Asn Glu Trp Gly Tyr Gln Glu Met Leu Met Tyr Gly Thr Gln Leu Gly	
305 310 315 320	

tgt act tgc cga aga tcg tgg gga tag	987
Cys Thr Cys Arg Arg Ser Trp Gly	
325	

<210> SEQ ID NO 8
<211> LENGTH: 328
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 8

Met Glu Lys Ala Leu Arg Asn Phe Thr Glu Ser Thr His Ser Pro Asp	
1 5 10 15	

Pro Asn Pro Leu Thr Lys Phe Phe Thr Glu Pro Thr Ala Ser Pro Val	
20 25 30	

Ser Arg Asn Arg Lys Leu Ser Ser Lys Asp Thr Thr Val Thr Ile Ala	
35 40 45	

Gly Ala Gly Ser Ser Thr Thr Arg Tyr Arg Gly Val Arg Arg Arg Pro	
50 55 60	

Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Met Ser Lys Glu Arg	
65 70 75 80	

Arg Trp Leu Gly Thr Phe Asp Thr Ala Glu Gln Ala Ala Cys Ala Tyr	
85 90 95	

Asp Ser Ala Ala Arg Ala Phe Arg Gly Ala Lys Ala Arg Thr Asn Phe	
100 105 110	

Thr Tyr Pro Thr Ala Val Ile Met Pro Glu Pro Arg Phe Ser Phe Ser	
115 120 125	

Asn Lys Lys Ser Ser Pro Ser Ala Arg Cys Pro Leu Pro Ser Leu Pro	
130 135 140	

Leu Asp Ser Ser Thr Gln Asn Phe Tyr Gly Ala Pro Ala Ala Gln Arg	
145 150 155 160	

Ile Tyr Asn Thr Gln Ser Ile Phe Leu Arg Asp Ala Ser Cys Ser Ser	
165 170 175	

Arg Lys Thr Thr Pro Tyr Asn Asn Ser Phe Asn Gly Ser Ser Ser Ser	
180 185 190	

Tyr Ser Ala Ser Lys Thr Ala Cys Val Ser Tyr Ser Glu Asn Glu Asn	
195 200 205	

Asn Glu Ser Phe Pro Glu Glu Ser Ser Asp Thr Gly Leu Leu Gln	
210 215 220	

Glu Val Val Gln Glu Phe Leu Lys Lys Asn Arg Gly Val Pro Pro Ser	
225 230 235 240	

Pro Pro Thr Pro Pro Val Thr Ser His His Asp Asn Ser Gly Tyr	
245 250 255	

Phe Ser Asn Leu Thr Ile Tyr Ser Glu Asn Met Val Gln Glu Thr Lys	
260 265 270	

Glu Thr Leu Ser Ser Lys Leu Asp Arg Tyr Gly Asn Phe Gln Ala Asn	
275 280 285	

Asp Asp Gly Val Arg Ala Val Ala Asp Gly Gly Leu Ser Leu Gly Ser	
290 295 300	

Asn Glu Trp Gly Tyr Gln Glu Met Leu Met Tyr Gly Thr Gln Leu Gly	
305 310 315 320	

Cys Thr Cys Arg Arg Ser Trp Gly	
325	

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<210> SEQ ID NO 9
<211> LENGTH: 1047
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1) ..(1047)

<400> SEQUENCE: 9

atg gaa agt ctc gca cac att cct ccc ggt tat cga ttc cat ccg acc	48
Met Glu Ser Leu Ala His Ile Pro Pro Gly Tyr Arg Phe His Pro Thr	
1 5 10 15	
gat gaa gaa ctc gtt gac tat tat ctc aag aac aaa gtt gca ttc ccg	96
Asp Glu Glu Leu Val Asp Tyr Tyr Leu Lys Asn Lys Val Ala Phe Pro	
20 25 30	
gga atg caa gtt gat gtt atc aaa gat gtt gat ctc tac aaa atc gag	144
Gly Met Gln Val Asp Val Ile Lys Asp Val Asp Leu Tyr Lys Ile Glu	
35 40 45	
cca tgg gac atc caa gag tta tgt gga aga ggg aca gga gaa gag agg	192
Pro Trp Asp Ile Gln Glu Leu Cys Gly Arg Gly Thr Gly Glu Glu Arg	
50 55 60	
gaa tgg tat ttc ttt agc cac aag gac aag aaa tat cca act ggg aca	240
Glu Trp Tyr Phe Ser His Lys Asp Lys Lys Tyr Pro Thr Gly Thr	
65 70 75 80	
cga acc aat aga gca acg ggc tcc gga ttt tgg aaa gca acg ggt cga	288
Arg Thr Asn Arg Ala Thr Gly Ser Gly Phe Trp Lys Ala Thr Gly Arg	
85 90 95	
gac aag gcc att tac tca aag caa gag ctt gtt ggg atg agg aag act	336
Asp Lys Ala Ile Tyr Ser Lys Gln Glu Leu Val Gly Met Arg Lys Thr	
100 105 110	
ctt gtc ttt tac aaa ggt agg gcc cca aat ggt cag aaa tct gat tgg	384
Leu Val Phe Tyr Lys Gly Arg Ala Pro Asn Gly Gln Lys Ser Asp Trp	
115 120 125	
ata atg cac gaa tac cgt ctt gag acc gat gaa aat gga ccg cct cat	432
Ile Met His Glu Tyr Arg Leu Glu Thr Asp Glu Asn Gly Pro Pro His	
130 135 140	
gag gaa gga tgg gtg gtt tgt cgc gct ttc aag aag aag cta acc acg	480
Glu Glu Gly Trp Val Val Cys Arg Ala Phe Lys Lys Lys Leu Thr Thr	
145 150 155 160	
atg aac tac aac aat cca aga aca atg atg gga tca tca tca ggc caa	528
Met Asn Tyr Asn Asn Pro Arg Thr Met Met Gly Ser Ser Gly Gln	
165 170 175	
gaa tct aac tgg ttc acg cag caa atg gat gtg ggg aat ggt aat tac	576
Glu Ser Asn Trp Phe Thr Gln Gln Met Asp Val Gly Asn Gly Asn Tyr	
180 185 190	
tat cat ctt cct gat cta gag agt ccg aga atg ttt caa ggc tca tca	624
Tyr His Leu Pro Asp Leu Glu Ser Pro Arg Met Phe Gln Gly Ser Ser	
195 200 205	
tca tca tca cta tca tca tta cat cag aat gat caa gac cct tat ggt	672
Ser Ser Ser Leu Ser Ser Leu His Gln Asn Asp Gln Asp Pro Tyr Gly	
210 215 220	
gtc gta ctc agc act att aac gca acc cca act aca ata atg caa cga	720
Val Val Leu Ser Thr Ile Asn Ala Thr Pro Thr Thr Ile Met Gln Arg	
225 230 235 240	
gat gat ggt cat gtg att acc aat gat gat gat cat atg atc atg atg	768
Asp Asp Gly His Val Ile Thr Asn Asp Asp Asp His Met Ile Met Met	
245 250 255	
aac aca agt act ggt gat cat cat caa tca gga tta cta gtc aat gat	816
Asn Thr Ser Thr Gly Asp His His Gln Ser Gly Leu Leu Val Asn Asp	
260 265 270	

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gat cat aat gat caa gta atg gat tgg caa acg ctt gac aag ttt gtt	864
Asp His Asn Asp Gln Val Met Asp Trp Gln Thr Leu Asp Lys Phe Val	
275 280 285	

gct tct cag cta atc atg agc caa gaa gag gaa gtt aac aaa gat	912
Ala Ser Gln Leu Ile Met Ser Gln Glu Glu Glu Val Asn Lys Asp	
290 295 300	

cca tca gat aat tct tcg aat gaa aca ttt cat cat ctc tct gaa gag	960
Pro Ser Asp Asn Ser Ser Asn Glu Thr Phe His His Leu Ser Glu Glu	
305 310 315 320	

caa gct gca aca atg gtt tcg atg aat gct tct tcc tct tct tct cca	1008
Gln Ala Ala Thr Met Val Ser Met Asn Ala Ser Ser Ser Ser Pro	
325 330 335	

tgt tcc ttc tac tct tgg gct caa aat aca cac acg taa	1047
Cys Ser Phe Tyr Ser Trp Ala Gln Asn Thr His Thr	
340 345	

<210> SEQ_ID NO 10

<211> LENGTH: 348

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 10

Met Glu Ser Leu Ala His Ile Pro Pro Gly Tyr Arg Phe His Pro Thr	
1 5 10 15	

Asp Glu Glu Leu Val Asp Tyr Tyr Leu Lys Asn Lys Val Ala Phe Pro	
20 25 30	

Gly Met Gln Val Asp Val Ile Lys Asp Val Asp Leu Tyr Lys Ile Glu	
35 40 45	

Pro Trp Asp Ile Gln Glu Leu Cys Gly Arg Gly Thr Gly Glu Glu Arg	
50 55 60	

Glu Trp Tyr Phe Phe Ser His Lys Asp Lys Lys Tyr Pro Thr Gly Thr	
65 70 75 80	

Arg Thr Asn Arg Ala Thr Gly Ser Gly Phe Trp Lys Ala Thr Gly Arg	
85 90 95	

Asp Lys Ala Ile Tyr Ser Lys Gln Glu Leu Val Gly Met Arg Lys Thr	
100 105 110	

Leu Val Phe Tyr Lys Gly Arg Ala Pro Asn Gly Gln Lys Ser Asp Trp	
115 120 125	

Ile Met His Glu Tyr Arg Leu Glu Thr Asp Glu Asn Gly Pro Pro His	
130 135 140	

Glu Glu Gly Trp Val Val Cys Arg Ala Phe Lys Lys Lys Leu Thr Thr	
145 150 155 160	

Met Asn Tyr Asn Asn Pro Arg Thr Met Met Gly Ser Ser Gly Gln	
165 170 175	

Glu Ser Asn Trp Phe Thr Gln Gln Met Asp Val Gly Asn Gly Asn Tyr	
180 185 190	

Tyr His Leu Pro Asp Leu Glu Ser Pro Arg Met Phe Gln Gly Ser Ser	
195 200 205	

Ser Ser Ser Leu Ser Ser Leu His Gln Asn Asp Gln Asp Pro Tyr Gly	
210 215 220	

Val Val Leu Ser Thr Ile Asn Ala Thr Pro Thr Thr Ile Met Gln Arg	
225 230 235 240	

Asp Asp Gly His Val Ile Thr Asn Asp Asp Asp His Met Ile Met Met	
245 250 255	

Asn Thr Ser Thr Gly Asp His His Gln Ser Gly Leu Leu Val Asn Asp	
260 265 270	

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Asp His Asn Asp Gln Val Met Asp Trp Gln Thr Leu Asp Lys Phe Val		
275	280	285

Ala Ser Gln Leu Ile Met Ser Gln Glu Glu Glu Val Asn Lys Asp		
290	295	300

Pro Ser Asp Asn Ser Ser Asn Glu Thr Phe His His Leu Ser Glu Glu			
305	310	315	320

Gln Ala Ala Thr Met Val Ser Met Asn Ala Ser Ser Ser Ser Pro		
325	330	335

Cys Ser Phe Tyr Ser Trp Ala Gln Asn Thr His Thr	
340	345

<210> SEQ ID NO 11

<211> LENGTH: 1032

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(1032)

<400> SEQUENCE: 11

atg gaa gcg gag aag aaa atg gtt cta ccg aga atc aaa ttc aca gag	48
Met Glu Ala Glu Lys Lys Met Val Leu Pro Arg Ile Lys Phe Thr Glu	
1 5 10 15	

cac aaa acc aac acg aca aca atc gta tcg gag tta acc aac act cac	96
His Lys Thr Asn Thr Thr Ile Val Ser Glu Leu Thr Asn Thr His	
20 25 30	

caa acc agg att ctt cgt atc tca gtc act gac cca gac gct act gat	144
Gln Thr Arg Ile Leu Arg Ile Ser Val Thr Asp Pro Asp Ala Thr Asp	
35 40 45	

tcc tcc agt gac gac gaa gaa gaa cat caa cgc ttt gtc tct aaa	192
Ser Ser Asp Asp Glu Glu Glu His Gln Arg Phe Val Ser Lys	
50 55 60	

cgc cgt cgt gtt aag aag ttt gtc aac gaa gtc tat ctc gat tcc ggt	240
Arg Arg Arg Val Lys Lys Phe Val Asn Glu Val Tyr Leu Asp Ser Gly	
65 70 75 80	

gct gtt gtt act ggt agt tgt ggt caa atg gag tcg aag aag aga caa	288
Ala Val Val Thr Gly Ser Cys Gly Gln Met Glu Ser Lys Lys Arg Gln	
85 90 95	

aag aga gcg gtt aaa tcg gag tct act gtt tct ccg gtt tca gcg	336
Lys Arg Ala Val Lys Ser Glu Ser Thr Val Ser Pro Val Val Ser Ala	
100 105 110	

acg acg act acg acg gga gag aag aag ttc cga gga gtg aga cag cgt	384
Thr Thr Thr Gly Glu Lys Phe Arg Gly Val Arg Gln Arg	
115 120 125	

cca tgg gga aaa tgg gcg gcg gag ata aga gat ccg ttg aaa cgt gta	432
Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Leu Lys Arg Val	
130 135 140	

cgg ctc tgg tta ggt act tac aac acg gcg gaa gaa gct gct atg gtt	480
Arg Leu Trp Leu Gly Thr Tyr Asn Thr Ala Glu Glu Ala Ala Met Val	
145 150 155 160	

tac gat aac gcc gct att cag ctt cgt ggt ccc gac gct ctg act aat	528
Tyr Asp Asn Ala Ala Ile Gln Leu Arg Gly Pro Asp Ala Leu Thr Asn	
165 170 175	

ttc tca gtc act ccg aca aca gcg acg gag aag aaa gcc cca cca ccg	576
Phe Ser Val Thr Pro Thr Ala Thr Glu Lys Lys Ala Pro Pro Pro	
180 185 190	

tct ccg gtg aag aag aag aag aaa aac aac aaa agc aaa aaa tcc	624
Ser Pro Val Lys Lys Lys Lys Lys Asn Asn Lys Ser Lys Lys Ser	
195 200 205	

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59**60**

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gtt act gct tct tcc tcc atc agc aga agc agc agc aac gat tgt ctc	672
Val Thr Ala Ser Ser Ser Ile Ser Arg Ser Ser Ser Asn Asp Cys Leu	
210 215 220	
 tgc tct ccg gtg tct ctc cga tct cct ttc gcc gtc gac gaa ttc	720
Cys Ser Pro Val Ser Val Leu Arg Ser Pro Phe Ala Val Asp Glu Phe	
225 230 235 240	
 tcc ggc att tct tca tca cca gtc gcg gtc gtt gta gtc aag gaa gag	768
Ser Gly Ile Ser Ser Pro Val Ala Ala Val Val Lys Glu Glu	
245 250 255	
 cca tcc atg aca acg gta tct gaa act ttc tct gat ttc tcg gcg ccc	816
Pro Ser Met Thr Thr Val Ser Glu Thr Phe Ser Asp Phe Ser Ala Pro	
260 265 270	
 ttg ttc tca gat gat gac gtg ttc gat ttc cgg agc tca gtg gtt ccc	864
Leu Phe Ser Asp Asp Asp Val Phe Asp Phe Arg Ser Ser Val Val Pro	
275 280 285	
 gac tat ctc ggc ggc gat tta ttt ggg gaa gat cta ttc acg gcg gat	912
Asp Tyr Leu Gly Gly Asp Leu Phe Gly Glu Asp Leu Phe Thr Ala Asp	
290 295 300	
 atg tgt acg gat atg aac ttc gga ttc gat ttc gga tcc gga tta tcc	960
Met Cys Thr Asp Met Asn Phe Gly Asp Phe Gly Ser Gly Leu Ser	
305 310 315 320	
 agc tgg cac atg gag gac cat ttt caa gat atc ggg gat cta ttc ggg	1008
Ser Trp His Met Glu Asp His Phe Gln Asp Ile Gly Asp Leu Phe Gly	
325 330 335	
 tcg gat cct ctt tta gct gtt taa	1032
Ser Asp Pro Leu Leu Ala Val	
340	

<210> SEQ_ID NO 12

<211> LENGTH: 343

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 12

Met Glu Ala Glu Lys Lys Met Val Leu Pro Arg Ile Lys Phe Thr Glu	
1 5 10 15	

His Lys Thr Asn Thr Thr Ile Val Ser Glu Leu Thr Asn Thr His	
20 25 30	

Gln Thr Arg Ile Leu Arg Ile Ser Val Thr Asp Pro Asp Ala Thr Asp	
35 40 45	

Ser Ser Ser Asp Asp Glu Glu Glu His Gln Arg Phe Val Ser Lys	
50 55 60	

Arg Arg Arg Val Lys Lys Phe Val Asn Glu Val Tyr Leu Asp Ser Gly	
65 70 75 80	

Ala Val Val Thr Gly Ser Cys Gly Gln Met Glu Ser Lys Lys Arg Gln	
85 90 95	

Lys Arg Ala Val Lys Ser Glu Ser Thr Val Ser Pro Val Val Ser Ala	
100 105 110	

Thr Thr Thr Thr Gly Glu Lys Phe Arg Gly Val Arg Gln Arg	
115 120 125	

Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Leu Lys Arg Val	
130 135 140	

Arg Leu Trp Leu Gly Thr Tyr Asn Thr Ala Glu Glu Ala Ala Met Val	
145 150 155 160	

Tyr Asp Asn Ala Ala Ile Gln Leu Arg Gly Pro Asp Ala Leu Thr Asn	
165 170 175	

Phe Ser Val Thr Pro Thr Ala Thr Glu Lys Lys Ala Pro Pro Pro	
180 185 190	

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Ser Pro Val Lys Lys Lys Lys Lys Asn Asn Lys Ser Lys Lys Ser
195 200 205

Val Thr Ala Ser Ser Ser Ile Ser Arg Ser Ser Asn Asp Cys Leu
210 215 220

Cys Ser Pro Val Ser Val Leu Arg Ser Pro Phe Ala Val Asp Glu Phe
225 230 235 240

Ser Gly Ile Ser Ser Ser Pro Val Ala Ala Val Val Val Lys Glu Glu
245 250 255

Pro Ser Met Thr Thr Val Ser Glu Thr Phe Ser Asp Phe Ser Ala Pro
260 265 270

Leu Phe Ser Asp Asp Asp Val Phe Asp Phe Arg Ser Ser Val Val Pro
275 280 285

Asp Tyr Leu Gly Gly Asp Leu Phe Gly Glu Asp Leu Phe Thr Ala Asp
290 295 300

Met Cys Thr Asp Met Asn Phe Gly Phe Asp Phe Gly Ser Gly Leu Ser
305 310 315 320

Ser Trp His Met Glu Asp His Phe Gln Asp Ile Gly Asp Leu Phe Gly
325 330 335

Ser Asp Pro Leu Leu Ala Val
340

<210> SEQ ID NO 13
<211> LENGTH: 666
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(666)

<400> SEQUENCE: 13

atg gcg gat tcg tct tcc gac aag gag aag aag gaa aat aat aag cag	48
Met Ala Asp Ser Ser Ser Asp Lys Glu Lys Lys Glu Asn Asn Lys Gln	
1 5 10 15	
ccc gtg tat cgt gga gtc cgt atg agg agc tgg gga aaa tgg gta tcg	96
Pro Val Tyr Arg Gly Val Arg Met Arg Ser Trp Gly Lys Trp Val Ser	
20 25 30	
gag att cgc gaa ccg agg aag aaa tcg aga atc tgg ctc ggg act ttt	144
Glu Ile Arg Glu Pro Arg Lys Ser Arg Ile Trp Leu Gly Thr Phe	
35 40 45	
ccg acg gcg gag atg gct atg cgt gct cac gac gtg gcg gct atg agt	192
Pro Thr Ala Glu Met Ala Met Arg Ala His Asp Val Ala Ala Met Ser	
50 55 60	
atc aaa gga act tca gcc att ctc aat ttc cct gag ctc tct aaa ctt	240
Ile Lys Gly Thr Ser Ala Ile Leu Asn Phe Pro Glu Leu Ser Lys Leu	
65 70 75 80	
ctt ccc cga ccc gtt tcg ctc agc cct cgt gac gtc aga gct gcg gcg	288
Leu Pro Arg Pro Val Ser Leu Ser Pro Arg Asp Val Arg Ala Ala Ala	
85 90 95	
acc aaa gct ctc atg gac ttc gat acg acg gcg ttt cgt tcg gat	336
Thr Lys Ala Ala Leu Met Asp Phe Asp Thr Thr Ala Phe Arg Ser Asp	
100 105 110	
act gag act agc gaa acg acg acg tcg aat aaa atg tca gag agt agt	384
Thr Glu Thr Ser Glu Thr Thr Ser Asn Lys Met Ser Glu Ser Ser	
115 120 125	
gag agt aac gaa acg gtg tcg ttc tca tcg tcg tct tgg tcc tct gtt	432
Glu Ser Asn Glu Thr Val Ser Phe Ser Ser Ser Trp Ser Ser Val	
130 135 140	

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acg agc att gag gaa agt aca gtc tcc gac gat ctt gac gag atc gta	480
Thr Ser Ile Glu Glu Ser Thr Val Ser Asp Asp Leu Asp Glu Ile Val	
145 150 155 160	

aag tta ccg agt cta gga acg agc cta aac gag tcg aac gag ttc gtg	528
Lys Leu Pro Ser Leu Gly Thr Ser Leu Asn Glu Ser Asn Glu Phe Val	
165 170 175	

ata ttt gac tcg ttg gag gat ttg gtg tac atg cct cgg tgg tta agc	576
Ile Phe Asp Ser Leu Glu Asp Leu Val Tyr Met Pro Arg Trp Leu Ser	
180 185 190	

ggt acg gaa gaa gtt ttt acg tat aat aac aat gat tct tcg ttg	624
Gly Thr Glu Glu Val Phe Thr Tyr Asn Asn Asn Asp Ser Ser Leu	
195 200 205	

aat tac tca tca gtt ttc gaa tct tgg aaa cat ttt ccc tga	666
Asn Tyr Ser Ser Val Phe Glu Ser Trp Lys His Phe Pro	
210 215 220	

<210> SEQ ID NO 14

<211> LENGTH: 221

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 14

Met Ala Asp Ser Ser Asp Lys Glu Lys Lys Glu Asn Asn Lys Gln	
1 5 10 15	

Pro Val Tyr Arg Gly Val Arg Met Arg Ser Trp Gly Lys Trp Val Ser	
20 25 30	

Glu Ile Arg Glu Pro Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe	
35 40 45	

Pro Thr Ala Glu Met Ala Met Arg Ala His Asp Val Ala Ala Met Ser	
50 55 60	

Ile Lys Gly Thr Ser Ala Ile Leu Asn Phe Pro Glu Leu Ser Lys Leu	
65 70 75 80	

Leu Pro Arg Pro Val Ser Leu Ser Pro Arg Asp Val Arg Ala Ala Ala	
85 90 95	

Thr Lys Ala Ala Leu Met Asp Phe Asp Thr Thr Ala Phe Arg Ser Asp	
100 105 110	

Thr Glu Thr Ser Glu Thr Thr Ser Asn Lys Met Ser Glu Ser Ser	
115 120 125	

Glu Ser Asn Glu Thr Val Ser Phe Ser Ser Ser Trp Ser Ser Val	
130 135 140	

Thr Ser Ile Glu Glu Ser Thr Val Ser Asp Asp Leu Asp Glu Ile Val	
145 150 155 160	

Lys Leu Pro Ser Leu Gly Thr Ser Leu Asn Glu Ser Asn Glu Phe Val	
165 170 175	

Ile Phe Asp Ser Leu Glu Asp Leu Val Tyr Met Pro Arg Trp Leu Ser	
180 185 190	

Gly Thr Glu Glu Val Phe Thr Tyr Asn Asn Asn Asp Ser Ser Leu	
195 200 205	

Asn Tyr Ser Ser Val Phe Glu Ser Trp Lys His Phe Pro	
210 215 220	

<210> SEQ ID NO 15

<211> LENGTH: 921

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1) .. (921)

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65

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66

<400> SEQUENCE: 15

atg gaa gaa gca atc atg aga ctc gaa ggt gcc gag cac aga gaa acc Met Glu Glu Ala Ile Met Arg Leu Glu Gly Ala Glu His Arg Glu Thr 1 5 10 15	48
aac atc cat tct ttg aaa aga aag cca tca aga act tcc tcg aca gct Asn Ile His Ser Leu Lys Arg Lys Pro Ser Arg Thr Ser Ser Thr Ala 20 25 30	96
cct ggc tct ccc gga gga gta act acc gca aaa gct gcc tcc ggc gcc Pro Gly Ser Pro Gly Gly Val Thr Thr Ala Lys Ala Ala Ser Gly Ala 35 40 45	144
ggc gct tcc ggt gtc tct acg ata agg tac cga ggc gtg agg cgt agg Gly Ala Ser Gly Val Ser Thr Ile Arg Tyr Arg Gly Val Arg Arg Arg 50 55 60	192
cca tgg ggt cgt tac gca gct gaa ata cgg gac cca ttg tcc aag gag Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Leu Ser Lys Glu 65 70 75 80	240
aga cga tgg ctc gga aca ttt gac acg gcc gag gaa gca gct tgc gca Arg Arg Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Cys Ala 85 90 95	288
tat gac tgc gcc gct cga gcc atg cgt ggt ctt aaa gct cga acc aac Tyr Asp Cys Ala Ala Arg Ala Met Arg Gly Leu Lys Ala Arg Thr Asn 100 105 110	336
ttc gtc tac cca atg cct tct ctc gac tct tat cac cac cgt att ttc Phe Val Tyr Pro Met Pro Ser Leu Asp Ser Tyr His His Arg Ile Phe 115 120 125	384
tcg tct cct cca atg aat atg ttc ctt cta cga gac gtg tta aac tct Ser Ser Pro Pro Met Asn Met Phe Leu Leu Arg Asp Val Leu Asn Ser 130 135 140	432
cag tct ctt ccg tta acc act ttc gct tac ccg cct tgt aat ctt Gln Ser Leu Ser Pro Leu Thr Thr Phe Ala Tyr Pro Pro Cys Asn Leu 145 150 155 160	480
tct aac gta aac gac gtt gtt cac gag tcc ttc act aac gtc aac gat Ser Asn Val Asn Asp Val Val His Glu Ser Phe Thr Asn Val Asn Asp 165 170 175	528
gtc tgt gaa gat ctc tcg cct aaa gct aag agg tca agt acc att gag Val Cys Glu Asp Leu Ser Pro Lys Ala Lys Arg Ser Ser Thr Ile Glu 180 185 190	576
aac gag agc ctg ata tca aat atc ttt gaa cca gaa cca gct agt tct Asn Glu Ser Leu Ile Ser Asn Ile Phe Glu Pro Glu Pro Ala Ser Ser 195 200 205	624
ggc ctt ctt caa gaa att gtt caa ggc ttc tta cca aaa cct atc tct Gly Leu Leu Gln Glu Ile Val Gln Gly Phe Leu Pro Lys Pro Ile Ser 210 215 220	672
caa cat gct tct ata cct cca aag agc aac caa cag tcg gtt ggt gtt Gln His Ala Ser Ile Pro Pro Lys Ser Asn Gln Gln Ser Val Gly Val 225 230 235 240	720
ttc ccg acg atg cca gag agc ggt ttt cag aca gat gtt cgt tta gct Phe Pro Thr Met Pro Glu Ser Gly Phe Gln Thr Asp Val Arg Leu Ala 245 250 255	768
gac ttc cat gtc gaa gga aac gga ttc ggt cag gtt aaa tat cat gga Asp Phe His Val Glu Gly Asn Gly Phe Gly Gln Val Lys Tyr His Gly 260 265 270	816
gag tta ggt tgg gct gat cat gag aat ggg ttt gat tca gct aag atg Glu Leu Gly Trp Ala Asp His Glu Asn Gly Phe Asp Ser Ala Lys Met 275 280 285	864
cag cag aac gga aat ggt gga atg ttt tat cag tat tgc ttt cat gat Gln Gln Asn Gly Asn Gly Gly Met Phe Tyr Gln Tyr Cys Phe His Asp 290 295 300	912
gat tat tag	921

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Asp Tyr
305

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<210> SEQ ID NO 16
<211> LENGTH: 306
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 16

Met Glu Ala Ile Met Arg Leu Glu Gly Ala Glu His Arg Glu Thr
1           5          10          15

Asn Ile His Ser Leu Lys Arg Lys Pro Ser Arg Thr Ser Ser Thr Ala
20          25          30

Pro Gly Ser Pro Gly Gly Val Thr Thr Ala Lys Ala Ala Ser Gly Ala
35          40          45

Gly Ala Ser Gly Val Ser Thr Ile Arg Tyr Arg Gly Val Arg Arg Arg
50          55          60

Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Leu Ser Lys Glu
65          70          75          80

Arg Arg Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Cys Ala
85          90          95

Tyr Asp Cys Ala Ala Arg Ala Met Arg Gly Leu Lys Ala Arg Thr Asn
100         105         110

Phe Val Tyr Pro Met Pro Ser Leu Asp Ser Tyr His His Arg Ile Phe
115         120         125

Ser Ser Pro Pro Met Asn Met Phe Leu Leu Arg Asp Val Leu Asn Ser
130         135         140

Gln Ser Leu Ser Pro Leu Thr Thr Phe Ala Tyr Pro Pro Cys Asn Leu
145         150         155         160

Ser Asn Val Asn Asp Val Val His Glu Ser Phe Thr Asn Val Asn Asp
165         170         175

Val Cys Glu Asp Leu Ser Pro Lys Ala Lys Arg Ser Ser Thr Ile Glu
180         185         190

Asn Glu Ser Leu Ile Ser Asn Ile Phe Glu Pro Glu Pro Ala Ser Ser
195         200         205

Gly Leu Leu Gln Glu Ile Val Gln Gly Phe Leu Pro Lys Pro Ile Ser
210         215         220

Gln His Ala Ser Ile Pro Pro Lys Ser Asn Gln Gln Ser Val Gly Val
225         230         235         240

Phe Pro Thr Met Pro Glu Ser Gly Phe Gln Thr Asp Val Arg Leu Ala
245         250         255

Asp Phe His Val Glu Gly Asn Gly Phe Gly Gln Val Lys Tyr His Gly
260         265         270

Glu Leu Gly Trp Ala Asp His Glu Asn Gly Phe Asp Ser Ala Lys Met
275         280         285

Gln Gln Asn Gly Asn Gly Met Phe Tyr Gln Tyr Cys Phe His Asp
290         295         300

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Asp Tyr
305

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<210> SEQ ID NO 17
<211> LENGTH: 1011
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1011)

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<400> SEQUENCE: 17

atg tca aga aag cca tgt tgt gta gaa gga ctg aag aaa gga gca Met Ser Arg Lys Pro Cys Cys Val Gly Glu Gly Leu Lys Lys Gly Ala 1 5 10 15	48
tgg act gcc gaa gaa gac aag aaa ctc atc tct tac att cat gaa cac Trp Thr Ala Glu Glu Asp Lys Lys Leu Ile Ser Tyr Ile His Glu His 20 25 30	96
ggt gaa gga ggc tgg cgt gac att ccc caa aaa gct gga cta aaa cga Gly Glu Gly Trp Arg Asp Ile Pro Gln Lys Ala Gly Leu Lys Arg 35 40 45	144
tgt gga aag agt tgt aga ttg cga tgg gct aac tat ttg aaa cct gac Cys Gly Lys Ser Cys Arg Leu Arg Trp Ala Asn Tyr Leu Lys Pro Asp 50 55 60	192
atc aag aga gga gag ttt agc tat gag gag gaa cag att atc atc atg Ile Lys Arg Gly Glu Phe Ser Tyr Glu Glu Gln Ile Ile Ile Met 65 70 75 80	240
cta cac gct tct cgc ggc aac aag tgg tca gtc ata gcg aga cat ttg Leu His Ala Ser Arg Gly Asn Lys Trp Ser Val Ile Ala Arg His Leu 85 90 95	288
ccc aaa aga aca gat aac gag att aag aac tac tgg aac acg cat ctc Pro Lys Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Leu 100 105 110	336
aaa aag ctc ctg atc gat aag gga atc gat ccc gtc acc cac aag cca Lys Lys Leu Leu Ile Asp Lys Gly Ile Asp Pro Val Thr His Lys Pro 115 120 125	384
ctt gcc tat gac tca aac ccg gat gag caa tcg caa tcg ggt tcc atc Leu Ala Tyr Asp Ser Asn Pro Asp Glu Gln Ser Gln Ser Gly Ser Ile 130 135 140	432
tct cca aag tct ctt cct cct tca agc tcc aaa aat gta ccg gag ata Ser Pro Lys Ser Leu Pro Pro Ser Ser Lys Asn Val Pro Glu Ile 145 150 155 160	480
acc agc agt gac gag aca ccg aaa tat gat gct tcc ttg agc tcc aag Thr Ser Ser Asp Glu Thr Pro Lys Tyr Asp Ala Ser Leu Ser Ser Lys 165 170 175	528
aaa cgt tgt ttt aag aga tcg agt tct aca tca aaa ctg tta aac aaa Lys Arg Cys Phe Lys Arg Ser Ser Thr Ser Lys Leu Leu Asn Lys 180 185 190	576
gtt gca gct agg gct tct tcc atg gga act ata cta ggc gcc tcc atc Val Ala Ala Arg Ala Ser Ser Met Gly Thr Ile Leu Gly Ala Ser Ile 195 200 205	624
gaa gga acc ttg atc agc tct aca ccg ttg tct tca tgt cta aat gat Glu Gly Thr Leu Ile Ser Ser Thr Pro Leu Ser Ser Cys Leu Asn Asp 210 215 220	672
gac ttt tct gaa aca agtcaa ttt cag atg gaa gaa ttt gat cca ttc Asp Phe Ser Glu Thr Ser Gln Phe Gln Met Glu Glu Phe Asp Pro Phe 225 230 235 240	720
tat cag tca tct gaa cac ata att gat cat atg aaa gaa gat atc agc Tyr Gln Ser Ser Glu His Ile Ile Asp His Met Lys Glu Asp Ile Ser 245 250 255	768
atc aac aat tcc gaa tac gat ttc tcg cag ttt ctc gag cag ttt agt Ile Asn Asn Ser Glu Tyr Asp Phe Ser Gln Phe Leu Glu Gln Phe Ser 260 265 270	816
aac aac gaa ggg gaa gaa gct gac aat act gga gga gga tat aac caa Asn Asn Glu Gly Glu Glu Ala Asp Asn Thr Gly Gly Tyr Asn Gln 275 280 285	864
gat ctt ctt atg tct gat gtc tca aca agc gtt gat gaa gac gag Asp Leu Leu Met Ser Asp Val Ser Ser Thr Ser Val Asp Glu Asp Glu 290 295 300	912

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atg atg caa aac ata act ggt tgg tca aat tat ctc ctt gac cat tcc	960
Met Met Gln Asn Ile Thr Gly Trp Ser Asn Tyr Leu Leu Asp His Ser	
305 310 315 320	

gat ttc aat tat gac acg agc caa gat tac gac gac aag aac ttc ata	1008
Asp Phe Asn Tyr Asp Thr Ser Gln Asp Tyr Asp Asp Lys Asn Phe Ile	
325 330 335	

tga	1011
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<210> SEQ ID NO 18

<211> LENGTH: 336

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 18

Met Ser Arg Lys Pro Cys Cys Val Gly Glu Gly Leu Lys Lys Gly Ala	
1 5 10 15	

Trp Thr Ala Glu Glu Asp Lys Lys Leu Ile Ser Tyr Ile His Glu His	
20 25 30	

Gly Glu Gly Gly Trp Arg Asp Ile Pro Gln Lys Ala Gly Leu Lys Arg	
35 40 45	

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ala Asn Tyr Leu Lys Pro Asp	
50 55 60	

Ile Lys Arg Gly Glu Phe Ser Tyr Glu Glu Gln Ile Ile Ile Met	
65 70 75 80	

Leu His Ala Ser Arg Gly Asn Lys Trp Ser Val Ile Ala Arg His Leu	
85 90 95	

Pro Lys Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Leu	
100 105 110	

Lys Lys Leu Leu Ile Asp Lys Gly Ile Asp Pro Val Thr His Lys Pro	
115 120 125	

Leu Ala Tyr Asp Ser Asn Pro Asp Glu Gln Ser Gln Ser Gly Ser Ile	
130 135 140	

Ser Pro Lys Ser Leu Pro Pro Ser Ser Ser Lys Asn Val Pro Glu Ile	
145 150 155 160	

Thr Ser Ser Asp Glu Thr Pro Lys Tyr Asp Ala Ser Leu Ser Ser Lys	
165 170 175	

Lys Arg Cys Phe Lys Arg Ser Ser Thr Ser Lys Leu Leu Asn Lys	
180 185 190	

Val Ala Ala Arg Ala Ser Ser Met Gly Thr Ile Leu Gly Ala Ser Ile	
195 200 205	

Glu Gly Thr Leu Ile Ser Ser Thr Pro Leu Ser Ser Cys Leu Asn Asp	
210 215 220	

Asp Phe Ser Glu Thr Ser Gln Phe Gln Met Glu Glu Phe Asp Pro Phe	
225 230 235 240	

Tyr Gln Ser Ser Glu His Ile Ile Asp His Met Lys Glu Asp Ile Ser	
245 250 255	

Ile Asn Asn Ser Glu Tyr Asp Phe Ser Gln Phe Leu Glu Gln Phe Ser	
260 265 270	

Asn Asn Glu Gly Glu Ala Asp Asn Thr Gly Gly Tyr Asn Gln	
275 280 285	

Asp Leu Leu Met Ser Asp Val Ser Ser Thr Ser Val Asp Glu Asp Glu	
290 295 300	

Met Met Gln Asn Ile Thr Gly Trp Ser Asn Tyr Leu Leu Asp His Ser	
305 310 315 320	

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Asp	Phe	Asn	Tyr	Asp
325				Thr Ser Gln Asp Tyr Asp Asp Lys Asn Phe Ile
				330 335

<210> SEQ ID NO 19
<211> LENGTH: 636
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(636)

<400> SEQUENCE: 19

atg	gct	cgt	gga	aag	att	cag	ctt	aag	agg	att	gag	aac	ccg	gtt	cac		48
Met	Ala	Arg	Gly	Lys	Ile	Gln	Leu	Lys	Arg	Ile	Glu	Asn	Pro	Val	His		
1					5			10		15							
aga	caa	gtg	act	ttt	tgc	aag	agg	aga	act	ggc	ctt	ctc	aag	aag	gct		96
Arg	Gln	Val	Thr	Phe	Cys	Lys	Arg	Arg	Thr	Gly	Leu	Leu	Lys	Lys	Ala		
20					25			30									
aag	gag	ctc	tct	gtg	ctc	tgt	gat	gcc	gag	atc	ggc	gtt	gtg	atc	ttc		144
Lys	Glu	Leu	Ser	Val	Leu	Cys	Asp	Ala	Glu	Ile	Gly	Val	Val	Ile	Phe		
35					40			45									
tct	cct	cag	ggc	aag	ctc	ttt	gag	ctc	gct	act	aaa	gga	aca	atg	gag		192
Ser	Pro	Gln	Gly	Lys	Leu	Phe	Glu	Leu	Ala	Thr	Lys	Gly	Thr	Met	Glu		
50					55			60									
gga	atg	att	gat	aag	tac	atg	aag	tgt	act	ggc	ggc	ggc	ggc	ggc	tct		240
Gly	Met	Ile	Asp	Lys	Tyr	Met	Lys	Cys	Thr	Gly	Gly	Gly	Gly	Arg	Gly	Ser	
65					70			75		80							
tct	tct	gct	act	ttt	act	gct	caa	gaa	caa	ctt	caa	cca	cca	aat	ctt		288
Ser	Ser	Ala	Thr	Phe	Thr	Ala	Gln	Glu	Gln	Leu	Gln	Pro	Pro	Asn	Leu		
85					90			95									
gat	ccg	aaa	gat	gag	atc	aac	gtg	ctt	aag	caa	gag	att	gag	atg	ctt		336
Asp	Pro	Lys	Asp	Glu	Ile	Asn	Val	Leu	Lys	Gln	Glu	Ile	Glu	Met	Leu		
100					105			110									
cag	aaa	ggg	ata	agc	tat	atg	ttt	gga	gga	gga	gat	ggg	gct	atg	aat		384
Gln	Lys	Gly	Ile	Ser	Tyr	Met	Phe	Gly	Gly	Gly	Asp	Gly	Ala	Met	Asn		
115					120			125									
ctt	gaa	gaa	ctt	ctt	ttg	ctt	gag	aag	cat	ctt	gag	tat	tgg	att	tct		432
Leu	Glu	Glu	Leu	Leu	Leu	Leu	Glu	Lys	His	Leu	Glu	Tyr	Trp	Ile	Ser		
130					135			140									
cag	att	cgc	tct	gct	aag	atg	gat	gtt	atg	ctt	caa	gaa	att	cag	tca		480
Gln	Ile	Arg	Ser	Ala	Lys	Met	Asp	Val	Met	Leu	Gln	Glu	Ile	Gln	Ser		
145					150			155		160							
ttg	agg	aac	aag	gaa	gga	gtc	ctc	aaa	aac	acc	aac	aag	tat	ctc	ctc		528
Leu	Arg	Asn	Lys	Glu	Gly	Val	Leu	Lys	Asn	Thr	Asn	Lys	Tyr	Leu	Leu		
165					170			175									
gaa	aag	ata	gag	gaa	aac	aac	aat	agc	ata	tta	gat	gct	aac	ttc	gca		576
Glu	Lys	Ile	Glu	Glu	Asn	Asn	Ser	Ile	Leu	Asp	Ala	Asn	Phe	Ala			
180					185			190									
gtc	atg	gag	aca	aac	tat	tcc	tat	ccg	cta	aca	atg	cca	agt	gaa	ata		624
Val	Met	Glu	Thr	Asn	Tyr	Ser	Tyr	Pro	Leu	Thr	Met	Pro	Ser	Glu	Ile		
195					200			205									
ttt	cag	ttc	tag													636	
Phe	Gln	Phe															
210																	

<210> SEQ ID NO 20
<211> LENGTH: 211
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 20

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Met Ala Arg Gly Lys Ile Gln Leu Lys Arg Ile Glu Asn Pro Val His
 1 5 10 15
 Arg Gln Val Thr Phe Cys Lys Arg Arg Thr Gly Leu Leu Lys Lys Ala
 20 25 30
 Lys Glu Leu Ser Val Leu Cys Asp Ala Glu Ile Gly Val Val Ile Phe
 35 40 45
 Ser Pro Gln Gly Lys Leu Phe Glu Leu Ala Thr Lys Gly Thr Met Glu
 50 55 60
 Gly Met Ile Asp Lys Tyr Met Lys Cys Thr Gly Gly Arg Gly Ser
 65 70 75 80
 Ser Ser Ala Thr Phe Thr Ala Gln Glu Gln Leu Gln Pro Pro Asn Leu
 85 90 95
 Asp Pro Lys Asp Glu Ile Asn Val Leu Lys Glu Ile Glu Met Leu
 100 105 110
 Gln Lys Gly Ile Ser Tyr Met Phe Gly Gly Asp Gly Ala Met Asn
 115 120 125
 Leu Glu Glu Leu Leu Leu Glu Lys His Leu Glu Tyr Trp Ile Ser
 130 135 140
 Gln Ile Arg Ser Ala Lys Met Asp Val Met Leu Gln Glu Ile Gln Ser
 145 150 155 160
 Leu Arg Asn Lys Glu Gly Val Leu Lys Asn Thr Asn Lys Tyr Leu Leu
 165 170 175
 Glu Lys Ile Glu Glu Asn Asn Ser Ile Leu Asp Ala Asn Phe Ala
 180 185 190
 Val Met Glu Thr Asn Tyr Ser Tyr Pro Leu Thr Met Pro Ser Glu Ile
 195 200 205
 Phe Gln Phe
 210

<210> SEQ ID NO 21
 <211> LENGTH: 2514
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(2514)

<400> SEQUENCE: 21

atg gca atg tct tgc aag gat ggt aag ttg gga tgg ttt gat aat ggg	48
Met Ala Met Ser Cys Lys Asp Gly Lys Leu Gly Cys Leu Asp Asn Gly	
1 5 10 15	
aag tat gtg agg tat aca cct gaa caa gtt gaa gca ctt gag agg ctt	96
Lys Tyr Val Arg Tyr Thr Pro Glu Gln Val Glu Ala Leu Glu Arg Leu	
20 25 30	
tat cat gac tgt cct aaa ccg agt tct att cgc cgt cag cag ttg atc	144
Tyr His Asp Cys Pro Lys Pro Ser Ser Ile Arg Arg Gln Gln Leu Ile	
35 40 45	
aga gag tgt cct att ctc tct aac att gag cct aaa cag atc aaa gtg	192
Arg Glu Cys Pro Ile Leu Ser Asn Ile Glu Pro Lys Gln Ile Lys Val	
50 55 60	
tgg ttt cag aac cga aga tgt aga gag aaa caa agg aaa gag gct tca	240
Trp Phe Gln Asn Arg Arg Cys Arg Glu Lys Gln Arg Lys Glu Ala Ser	
65 70 75 80	
cgg ctt caa gct gtg aat cgg aag ttg acg gca atg aac aag ctc ttg	288
Arg Leu Gln Ala Val Asn Arg Lys Leu Thr Ala Met Asn Lys Leu Leu	
85 90 95	

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atg gag gag aat gac agg ttg cag aag caa gtg tca cag ctg gtc cat Met Glu Glu Asn Asp Arg Leu Gln Lys Gln Val Ser Gln Leu Val His 100 105 110	336
gaa aac agc tac ttc cgt caa cat act cca aat cct tca ctc cca gct Glu Asn Ser Tyr Phe Arg Gln His Thr Pro Asn Pro Ser Leu Pro Ala 115 120 125	384
aaa gac aca agc tgt gaa tcg gtg acg agt ggt cag cac caa ttg Lys Asp Thr Ser Cys Glu Ser Val Val Thr Ser Gly Gln His Gln Leu 130 135 140	432
gca tct caa aat cct cag aga gat gct agt cct gca gga ctt ttg tcc Ala Ser Gln Asn Pro Gln Arg Asp Ala Ser Pro Ala Gly Leu Leu Ser 145 150 155 160	480
att gca gaa gaa act tta gca gag ttt ctt tca aag gca act gga acc Ile Ala Glu Glu Thr Leu Ala Glu Phe Leu Ser Lys Ala Thr Gly Thr 165 170 175	528
gct gtt gag tgg gtt cag atg cct gga atg aag cct ggt ccg gat tcc Ala Val Glu Trp Val Gln Met Pro Gly Met Lys Pro Gly Pro Asp Ser 180 185 190	576
att gga atc atc gct att tct cat ggt tgc act ggt gtg gca gca cgc Ile Gly Ile Ile Ala Ile Ser His Gly Cys Thr Gly Val Ala Ala Arg 195 200 205	624
gcc tgt ggc cta gtg ggt ctt gag cct aca agg gtt gca gag att gtc Ala Cys Gly Leu Val Gly Leu Glu Pro Thr Arg Val Ala Glu Ile Val 210 215 220	672
aag gat cgt cct tcg tgg ttc cgc gaa tgg cgt cga gct gtt gaa gtt atg Lys Asp Arg Pro Ser Trp Phe Arg Glu Cys Arg Ala Val Glu Val Met 225 230 235 240	720
aac gtg ttg cca act gcc aat ggt gga acc gtt gag ctg ctt tat atg Asn Val Leu Pro Thr Ala Asn Gly Thr Val Glu Leu Leu Tyr Met 245 250 255	768
cag ctc tat gca cca act aca ttg gcc cca cca cgc gat ttc tgg ctg Gln Leu Tyr Ala Pro Thr Leu Ala Pro Pro Arg Asp Phe Trp Leu 260 265 270	816
tta cgt tac acc tct gtt tta gaa gat ggc agc ctt gtg gtc gag Leu Arg Tyr Thr Ser Val Leu Glu Asp Gly Ser Leu Val Val Cys Glu 275 280 285	864
aga tct ctt aag agc actcaa aat ggt cct agt atg cca ctg gtt cag Arg Ser Leu Lys Ser Thr Gln Asn Gly Pro Ser Met Pro Leu Val Gln 290 295 300	912
aat ttt gtg aga gca gag atg ctt tcc agt ggg tac ttg ata cgg cct Asn Phe Val Arg Ala Glu Met Leu Ser Ser Gly Tyr Leu Ile Arg Pro 305 310 315 320	960
tgt gat ggt ggc tca atc ata cac ata gtg gat cat atg gat ttg Cys Asp Gly Gly Ser Ile Ile His Ile Val Asp His Met Asp Leu 325 330 335	1008
gag gct tgt agc gtg cct gag gtc ttg cgc ccg ctc tat gag tca ccc Glu Ala Cys Ser Val Pro Glu Val Leu Arg Pro Leu Tyr Glu Ser Pro 340 345 350	1056
aaa gta ctt gca cag aac aca atg gcg gca ctg cgt cag ctc aag Lys Val Leu Ala Gln Lys Thr Thr Met Ala Ala Leu Arg Gln Leu Lys 355 360 365	1104
caa ata gct cag gag gtt act cag act aat agt agt gtt aat ggg tgg Gln Ile Ala Gln Glu Val Thr Gln Thr Asn Ser Ser Val Asn Gly Trp 370 375 380	1152
gga cgg cgt cct gct gcc tta aga gct ctc agc cag agg cta agc aga Gly Arg Arg Pro Ala Ala Leu Arg Ala Leu Ser Gln Arg Leu Ser Arg 385 390 395 400	1200
ggc ttc aat gaa gct gta aat ggt ttc act gat gaa gga tgg tca gtg Gly Phe Asn Glu Ala Val Asn Gly Phe Thr Asp Glu Gly Trp Ser Val 405 410 415	1248

ata gga gat agc atg gat gat gtc aca atc act gta aac tct tct cca Ile Gly Asp Ser Met Asp Asp Val Thr Ile Thr Val Val Asn Ser Ser Pro 420 425 430	1296
gac aag cta atg ggt cta aat ctt aca ttt gcc aat ggc ttt gct cct Asp Lys Leu Met Gly Leu Asn Leu Thr Phe Ala Asn Gly Phe Ala Pro 435 440 445	1344
gta agc aat gtt gtt tta tgc gca aaa gca tca atg ctt tta cag aat Val Ser Asn Val Val Leu Cys Ala Lys Ala Ser Met Leu Leu Gln Asn 450 455 460	1392
gtt cct ccg gcg atc ctg ctt cgg ttt ctg agg gag cat agg tca gaa Val Pro Pro Ala Ile Leu Leu Arg Phe Leu Arg Glu His Arg Ser Glu 465 470 475 480	1440
tgg gct gac aac aac att gat gcg tat cta gca gca gca gtt aaa gta Trp Ala Asp Asn Asn Ile Asp Ala Tyr Leu Ala Ala Val Lys Val 485 490 495	1488
ggg cct tgt agt gcc cga gtt gga gga ttt gga ggg cag gtt ata ctt Gly Pro Cys Ser Ala Arg Val Gly Gly Phe Gly Gly Gln Val Ile Leu 500 505 510	1536
cca ctt gct cat act att gag cat gaa gag ttt atg gaa gtc atc aaa Pro Leu Ala His Thr Ile Glu His Glu Glu Phe Met Glu Val Ile Lys 515 520 525	1584
ttg gaa ggt ctt ggt cat tcc cct gaa gat gca atc gtt cca aga gat Leu Glu Gly Leu Gly His Ser Pro Glu Asp Ala Ile Val Pro Arg Asp 530 535 540	1632
atc ttc ctt ctt caa ctt tgt agc gga atg gat gaa aat gct gta gga Ile Phe Leu Leu Gln Leu Cys Ser Gly Met Asp Glu Asn Ala Val Gly 545 550 555 560	1680
acc tgt gcg gaa ctt ata ttt gct cca atc gat gct tcg ttt gcg gat Thr Cys Ala Glu Leu Ile Phe Ala Pro Ile Asp Ala Ser Phe Ala Asp 565 570 575	1728
gat gca cct ctg ctt cct tct ggt ttt cgt att atc cct ctt gat tcc Asp Ala Pro Leu Leu Pro Ser Gly Phe Arg Ile Ile Pro Leu Asp Ser 580 585 590	1776
gca aag cag gaa gta tct agc cca aac cga acc ttg gat ctt gct tcg Ala Lys Gln Glu Val Ser Ser Pro Asn Arg Thr Leu Asp Leu Ala Ser 595 600 605	1824
gca ctg gaa att ggt tca gct gga aca aaa gcc tca act gat caa tca Ala Leu Glu Ile Gly Ser Ala Gly Thr Lys Ala Ser Thr Asp Gln Ser 610 615 620	1872
gga aac tcc aca tgt gca aga tct gtg atg aca ata gca ttt gag ttt Gly Asn Ser Thr Cys Ala Arg Ser Val Met Thr Ile Ala Phe Glu Phe 625 630 635 640	1920
ggc atc gag agc cat atg caa gaa cat gta gca tcc atg gct agg cag Gly Ile Glu Ser His Met Gln Glu His Val Ala Ser Met Ala Arg Gln 645 650 655	1968
tat gtt cga ggt atc ata tca tcg gtg cag aga gta gca ttg gct ctt Tyr Val Arg Gly Ile Ile Ser Ser Val Gln Arg Val Ala Leu Ala Leu 660 665 670	2016
tct cct tct cat atc agc tca caa gtt ggt cta cgc act cct ttg ggt Ser Pro Ser His Ile Ser Ser Gln Val Gly Leu Arg Thr Pro Leu Gly 675 680 685	2064
act cct gaa gcc caa aca ctt gct cgt tgg att tcg cag agt tac agg Thr Pro Glu Ala Gln Thr Leu Ala Arg Trp Ile Cys Gln Ser Tyr Arg 690 695 700	2112
ggc tac atg ggt gtt gag cta ctt aaa tca aac agt gac ggc aat gaa Gly Tyr Met Gly Val Glu Leu Leu Lys Ser Asn Ser Asp Gly Asn Glu 705 710 715 720	2160

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tct att ctt aag aat ctt tgg cat cac act gat gct ata atc tgc tgc Ser Ile Leu Lys Asn Leu Trp His His Thr Asp Ala Ile Ile Cys Cys 725 730 735	2208
tca atg aag gcc ttg ccc gtc ttc aca ttt gca aac cag gcg gga ctt Ser Met Lys Ala Leu Pro Val Phe Thr Phe Ala Asn Gln Ala Gly Leu 740 745 750	2256
gac atg ctg gag act aca tta gtt gct ctt caa gac atc tct tta gag Asp Met Leu Glu Thr Thr Leu Val Ala Leu Gln Asp Ile Ser Leu Glu 755 760 765	2304
aag ata ttt gat gac aat gga aga aag act ctt tgc tct gag ttc cca Lys Ile Phe Asp Asp Asn Gly Arg Lys Thr Leu Cys Ser Glu Phe Pro 770 775 780	2352
cag atc atg caa cag ggc ttc gcg tgc ctt caa ggc ggg ata tgg ctc Gln Ile Met Gln Gln Gly Phe Ala Cys Leu Gln Gly Ile Cys Leu 785 790 795 800	2400
tca agc atg ggg aga cca gtt tcg tat gag aga gca gtt gct tgg aaa Ser Ser Met Gly Arg Pro Val Ser Tyr Glu Arg Ala Val Ala Trp Lys 805 810 815	2448
gta ctc aat gaa gaa gaa aat gct cat tgc atc tgc ttt gtg ttc atc Val Leu Asn Glu Glu Glu Asn Ala His Cys Ile Cys Phe Val Phe Ile 820 825 830	2496
aat tgg tcc ttt gtg tga Asn Trp Ser Phe Val 835	2514

<210> SEQ ID NO 22
<211> LENGTH: 837
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 22

Met Ala Met Ser Cys Lys Asp Gly Lys Leu Gly Cys Leu Asp Asn Gly 1 5 10 15
Lys Tyr Val Arg Tyr Thr Pro Glu Gln Val Glu Ala Leu Glu Arg Leu 20 25 30
Tyr His Asp Cys Pro Lys Pro Ser Ser Ile Arg Arg Gln Gln Leu Ile 35 40 45
Arg Glu Cys Pro Ile Leu Ser Asn Ile Glu Pro Lys Gln Ile Lys Val 50 55 60
Trp Phe Gln Asn Arg Arg Cys Arg Glu Lys Gln Arg Lys Glu Ala Ser 65 70 75 80
Arg Leu Gln Ala Val Asn Arg Lys Leu Thr Ala Met Asn Lys Leu Leu 85 90 95
Met Glu Glu Asn Asp Arg Leu Gln Lys Gln Val Ser Gln Leu Val His 100 105 110
Glu Asn Ser Tyr Phe Arg Gln His Thr Pro Asn Pro Ser Leu Pro Ala 115 120 125
Lys Asp Thr Ser Cys Glu Ser Val Val Thr Ser Gly Gln His Gln Leu 130 135 140
Ala Ser Gln Asn Pro Gln Arg Asp Ala Ser Pro Ala Gly Leu Leu Ser 145 150 155 160
Ile Ala Glu Glu Thr Leu Ala Glu Phe Leu Ser Lys Ala Thr Gly Thr 165 170 175
Ala Val Glu Trp Val Gln Met Pro Gly Met Lys Pro Gly Pro Asp Ser 180 185 190
Ile Gly Ile Ile Ala Ile Ser His Gly Cys Thr Gly Val Ala Ala Arg 195 200 205

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Ala Cys Gly Leu Val Gly Leu Glu Pro Thr Arg Val Ala Glu Ile Val
 210 215 220

Lys Asp Arg Pro Ser Trp Phe Arg Glu Cys Arg Ala Val Glu Val Met
 225 230 235 240

Asn Val Leu Pro Thr Ala Asn Gly Gly Thr Val Glu Leu Leu Tyr Met
 245 250 255

Gln Leu Tyr Ala Pro Thr Thr Leu Ala Pro Pro Arg Asp Phe Trp Leu
 260 265 270

Leu Arg Tyr Thr Ser Val Leu Glu Asp Gly Ser Leu Val Val Cys Glu
 275 280 285

Arg Ser Leu Lys Ser Thr Gln Asn Gly Pro Ser Met Pro Leu Val Gln
 290 295 300

Asn Phe Val Arg Ala Glu Met Leu Ser Ser Gly Tyr Leu Ile Arg Pro
 305 310 315 320

Cys Asp Gly Gly Ser Ile Ile His Ile Val Asp His Met Asp Leu
 325 330 335

Glu Ala Cys Ser Val Pro Glu Val Leu Arg Pro Leu Tyr Glu Ser Pro
 340 345 350

Lys Val Leu Ala Gln Lys Thr Thr Met Ala Ala Leu Arg Gln Leu Lys
 355 360 365

Gln Ile Ala Gln Glu Val Thr Gln Thr Asn Ser Ser Val Asn Gly Trp
 370 375 380

Gly Arg Arg Pro Ala Ala Leu Arg Ala Leu Ser Gln Arg Leu Ser Arg
 385 390 395 400

Gly Phe Asn Glu Ala Val Asn Gly Phe Thr Asp Glu Gly Trp Ser Val
 405 410 415

Ile Gly Asp Ser Met Asp Asp Val Thr Ile Thr Val Asn Ser Ser Pro
 420 425 430

Asp Lys Leu Met Gly Leu Asn Leu Thr Phe Ala Asn Gly Phe Ala Pro
 435 440 445

Val Ser Asn Val Val Leu Cys Ala Lys Ala Ser Met Leu Leu Gln Asn
 450 455 460

Val Pro Pro Ala Ile Leu Leu Arg Phe Leu Arg Glu His Arg Ser Glu
 465 470 475 480

Trp Ala Asp Asn Asn Ile Asp Ala Tyr Leu Ala Ala Ala Val Lys Val
 485 490 495

Gly Pro Cys Ser Ala Arg Val Gly Gly Phe Gly Gln Val Ile Leu
 500 505 510

Pro Leu Ala His Thr Ile Glu His Glu Glu Phe Met Glu Val Ile Lys
 515 520 525

Leu Glu Gly Leu Gly His Ser Pro Glu Asp Ala Ile Val Pro Arg Asp
 530 535 540

Ile Phe Leu Leu Gln Leu Cys Ser Gly Met Asp Glu Asn Ala Val Gly
 545 550 555 560

Thr Cys Ala Glu Leu Ile Phe Ala Pro Ile Asp Ala Ser Phe Ala Asp
 565 570 575

Asp Ala Pro Leu Leu Pro Ser Gly Phe Arg Ile Ile Pro Leu Asp Ser
 580 585 590

Ala Lys Gln Glu Val Ser Ser Pro Asn Arg Thr Leu Asp Leu Ala Ser
 595 600 605

Ala Leu Glu Ile Gly Ser Ala Gly Thr Lys Ala Ser Thr Asp Gln Ser
 610 615 620

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Gly Asn Ser Thr Cys Ala Arg Ser Val Met Thr Ile Ala Phe Glu Phe
625 630 635 640

Gly Ile Glu Ser His Met Gln Glu His Val Ala Ser Met Ala Arg Gln
645 650 655

Tyr Val Arg Gly Ile Ile Ser Ser Val Gln Arg Val Ala Leu Ala Leu
660 665 670

Ser Pro Ser His Ile Ser Ser Gln Val Gly Leu Arg Thr Pro Leu Gly
675 680 685

Thr Pro Glu Ala Gln Thr Leu Ala Arg Trp Ile Cys Gln Ser Tyr Arg
690 695 700

Gly Tyr Met Gly Val Glu Leu Leu Lys Ser Asn Ser Asp Gly Asn Glu
705 710 715 720

Ser Ile Leu Lys Asn Leu Trp His His Thr Asp Ala Ile Ile Cys Cys
725 730 735

Ser Met Lys Ala Leu Pro Val Phe Thr Phe Ala Asn Gln Ala Gly Leu
740 745 750

Asp Met Leu Glu Thr Thr Leu Val Ala Leu Gln Asp Ile Ser Leu Glu
755 760 765

Lys Ile Phe Asp Asp Asn Gly Arg Lys Thr Leu Cys Ser Glu Phe Pro
770 775 780

Gln Ile Met Gln Gln Gly Phe Ala Cys Leu Gln Gly Ile Cys Leu
785 790 795 800

Ser Ser Met Gly Arg Pro Val Ser Tyr Glu Arg Ala Val Ala Trp Lys
805 810 815

Val Leu Asn Glu Glu Asn Ala His Cys Ile Cys Phe Val Phe Ile
820 825 830

Asn Trp Ser Phe Val
835

<210> SEQ ID NO 23
<211> LENGTH: 999
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(999)

<400> SEQUENCE: 23

atg gct gaa cga aag aaa cgc tct tct att caa acc aat aaa ccc aac	48
Met Ala Glu Arg Lys Lys Arg Ser Ser Ile Gln Thr Asn Lys Pro Asn	
1 5 10 15	
aaa aaa ccc atg aag aag aaa cct ttt cag cta aat cac ctc cca ggt	96
Lys Lys Pro Met Lys Lys Pro Phe Gln Leu Asn His Leu Pro Gly	
20 25 30	
tta tct gaa gat ttg aag act atg aga aaa ctc cgt ttc gtt gtg aat	144
Leu Ser Glu Asp Leu Lys Thr Met Arg Lys Leu Arg Phe Val Val Asn	
35 40 45	
gat cct tac gct act gac tac tca tca agc gaa gaa gaa agg agt	192
Asp Pro Tyr Ala Thr Asp Tyr Ser Ser Ser Glu Glu Glu Arg Ser	
50 55 60	
cag aga agg aaa cgt tat gtc tgt gag atc gat ctt cct ttc gct caa	240
Gln Arg Arg Lys Arg Tyr Val Cys Glu Ile Asp Leu Pro Phe Ala Gln	
65 70 75 80	
gct gct actcaa gca gaa tct gaa agc tca tat tgt cag gag agt aac	288
Ala Ala Thr Gln Ala Glu Ser Glu Ser Ser Tyr Cys Gln Glu Ser Asn	
85 90 95	

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aat aat ggt gta agc aag act aaa atc tca gct tgt agc aaa aag gtt Asn Asn Gly Val Ser Lys Thr Lys Ile Ser Ala Cys Ser Lys Lys Val 100 105 110	336
tta cgc agc aaa gca tct ccg gtc gtt gga cgt tct tct act act gtc Leu Arg Ser Lys Ala Ser Pro Val Val Gly Arg Ser Ser Thr Thr Val 115 120 125	384
tcg aag cct gtt ggt gtt agg cag agg aaa tgg ggt aaa tgg gct gct Ser Lys Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys Trp Ala Ala 130 135 140	432
gag att aga cat cca atc acc aaa gta aga act tgg ttg ggt act tac Glu Ile Arg His Pro Ile Thr Lys Val Arg Thr Trp Leu Gly Thr Tyr 145 150 155 160	480
gag acg ctt gaa caa gca gct gat gct tat gct acc aag aag ctt gag Glu Thr Leu Glu Gln Ala Ala Asp Ala Tyr Ala Thr Lys Lys Leu Glu 165 170 175	528
ttt gat gct ctg gct gca gcc act tct gct gct tcc tct gtt ttg tca Phe Asp Ala Leu Ala Ala Ala Thr Ser Ala Ala Ser Ser Val Leu Ser 180 185 190	576
aat gag tct ggt tct atg atc tca gcc tca ggg tca agc att gat ctt Asn Glu Ser Gly Ser Met Ile Ser Ala Ser Gly Ser Ser Ile Asp Leu 195 200 205	624
gac aag aag cta gtt gat tcg act ctt gat caa caa gct ggt gaa tcg Asp Lys Lys Leu Val Asp Ser Thr Leu Asp Gln Gln Ala Gly Glu Ser 210 215 220	672
aag aaa gcg agt ttt gat ttc gac ttt gca gat cta cag att cct gaa Lys Lys Ala Ser Phe Asp Phe Asp Phe Ala Asp Leu Gln Ile Pro Glu 225 230 235 240	720
atg ggt tgc ttc att gat gac tca ttc atc cca aat gct tgt gag ctt Met Gly Cys Phe Ile Asp Asp Ser Phe Ile Pro Asn Ala Cys Glu Leu 245 250 255	768
gat ttt ctc tta aca gaa gag aac aac aac caa atg ttg gat gat tac Asp Phe Leu Thr Glu Glu Asn Asn Asn Gln Met Leu Asp Asp Tyr 260 265 270	816
tgt ggc ata gat gat ctg gac atc att ggt ctt gaa tgt gac ggt cca Cys Gly Ile Asp Asp Leu Asp Ile Ile Gly Leu Glu Cys Asp Gly Pro 275 280 285	864
agc gaa ctt cca gac tat gat ttc tca gat gtg gag atc gat ctt ggt Ser Glu Leu Pro Asp Tyr Asp Phe Ser Asp Val Glu Ile Asp Leu Gly 290 295 300	912
ctc att gga acc acc att gac aag tat gct ttc gtt gat cat atc gca Leu Ile Gly Thr Thr Ile Asp Lys Tyr Ala Phe Val Asp His Ile Ala 305 310 315 320	960
aca act act ccc act cct ctt aat atc gcg tgc cca taa Thr Thr Thr Pro Thr Pro Leu Asn Ile Ala Cys Pro 325 330	999

<210> SEQ ID NO 24

<211> LENGTH: 332

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 24

Met Ala Glu Arg Lys Lys Arg Ser Ser Ile Gln Thr Asn Lys Pro Asn
1 5 10 15Lys Lys Pro Met Lys Lys Pro Phe Gln Leu Asn His Leu Pro Gly
20 25 30Leu Ser Glu Asp Leu Lys Thr Met Arg Lys Leu Arg Phe Val Val Asn
35 40 45Asp Pro Tyr Ala Thr Asp Tyr Ser Ser Ser Glu Glu Glu Arg Ser
50 55 60

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Gln Arg Arg Lys Arg Tyr Val Cys Glu Ile Asp Leu Pro Phe Ala Gln
65 70 75 80

Ala Ala Thr Gln Ala Glu Ser Glu Ser Ser Tyr Cys Gln Glu Ser Asn
85 90 95

Asn Asn Gly Val Ser Lys Thr Lys Ile Ser Ala Cys Ser Lys Lys Val
100 105 110

Leu Arg Ser Lys Ala Ser Pro Val Val Gly Arg Ser Ser Thr Thr Val
115 120 125

Ser Lys Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys Trp Ala Ala
130 135 140

Glu Ile Arg His Pro Ile Thr Lys Val Arg Thr Trp Leu Gly Thr Tyr
145 150 155 160

Glu Thr Leu Glu Gln Ala Ala Asp Ala Tyr Ala Thr Lys Lys Leu Glu
165 170 175

Phe Asp Ala Leu Ala Ala Ala Thr Ser Ala Ala Ser Ser Val Leu Ser
180 185 190

Asn Glu Ser Gly Ser Met Ile Ser Ala Ser Gly Ser Ser Ile Asp Leu
195 200 205

Asp Lys Lys Leu Val Asp Ser Thr Leu Asp Gln Gln Ala Gly Glu Ser
210 215 220

Lys Lys Ala Ser Phe Asp Phe Asp Phe Ala Asp Leu Gln Ile Pro Glu
225 230 235 240

Met Gly Cys Phe Ile Asp Asp Ser Phe Ile Pro Asn Ala Cys Glu Leu
245 250 255

Asp Phe Leu Leu Thr Glu Glu Asn Asn Asn Gln Met Leu Asp Asp Tyr
260 265 270

Cys Gly Ile Asp Asp Leu Asp Ile Ile Gly Leu Glu Cys Asp Gly Pro
275 280 285

Ser Glu Leu Pro Asp Tyr Asp Phe Ser Asp Val Glu Ile Asp Leu Gly
290 295 300

Leu Ile Gly Thr Thr Ile Asp Lys Tyr Ala Phe Val Asp His Ile Ala
305 310 315 320

Thr Thr Thr Pro Thr Pro Leu Asn Ile Ala Cys Pro
325 330

<210> SEQ ID NO 25
<211> LENGTH: 1101
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1101)

<400> SEQUENCE: 25

atg ggg aga cat tct tgc tgt tac aaa caa aag ctg agg aaa ggg ctt	48
Met Gly Arg His Ser Cys Cys Tyr Lys Gln Lys Leu Arg Lys Gly Leu	
1 5 10 15	
tgg tct cct gaa gaa gac gag aag ctt ctt act cac atc acc aat cac	96
Trp Ser Pro Glu Glu Asp Glu Lys Leu Leu Thr His Ile Thr Asn His	
20 25 30	
ggc cat ggc tgc tgg agc tct gtc cct aaa ctc gct ggt ttg cag aga	144
Gly His Cys Trp Ser Ser Val Pro Lys Leu Ala Gly Leu Gln Arg	
35 40 45	
tgt ggg aag agt tgg cga cta aga tgg atc aat tac ttg aga cct gat	192
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp	
50 55 60	

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tta aag aga gga gct ttt tct cct gaa gaa gag aat ctc atc gtc gaa Leu Lys Arg Gly Ala Phe Ser Pro Glu Glu Glu Asn Leu Ile Val Glu 65 70 75 80	240
ctt cat gcc gtc ctt gga aac aga tgg tca cag att gcg tca agg ctt Leu His Ala Val Leu Gly Asn Arg Trp Ser Gln Ile Ala Ser Arg Leu 85 90 95	288
ccg ggt aga acc gac aac gag atc aag aat cta tgg aac tca agc atc Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Leu Trp Asn Ser Ser Ile 100 105 110	336
aag aag aaa ctg aaa caa aga ggc att gac cca aac aca cac aag ccc Lys Lys Lys Leu Lys Gln Arg Gly Ile Asp Pro Asn Thr His Lys Pro 115 120 125	384
atc tct gaa gtt gag agt ttt agc gac aaa gac aaa cca aca aca agc Ile Ser Glu Val Glu Ser Phe Ser Asp Lys Asp Lys Pro Thr Thr Ser 130 135 140	432
aac aac aaa aga agc ggt aac gat cac aag tct cct agt tcc tct tct Asn Asn Lys Arg Ser Gly Asn Asp His Lys Ser Pro Ser Ser Ser 145 150 155 160	480
gcg act aac caa gac ttc ttc ctc gaa agg cca tct gat tta tcc gac Ala Thr Asn Gln Asp Phe Leu Glu Arg Pro Ser Asp Leu Ser Asp 165 170 175	528
tac ttc gga ttt cag aag ctt aac ttc aat cta gga ctc tct Tyr Phe Gly Phe Gln Lys Leu Asn Phe Asn Ser Asn Leu Gly Leu Ser 180 185 190	576
gtt aca act gat tct tca ctc tgc tcg atg att ccg ccg cag ttt agc Val Thr Thr Asp Ser Ser Leu Cys Ser Met Ile Pro Pro Gln Phe Ser 195 200 205	624
ccc ggg aac atg gtt ggt tct gtc ctt cag aca cca gta tgc gta aag Pro Gly Asn Met Val Gly Ser Val Leu Gln Thr Pro Val Cys Val Lys 210 215 220	672
ccc tcg att agt ctt cct ccc gac aac aac agt tcg agt cct atc tcc Pro Ser Ile Ser Leu Pro Pro Asp Asn Asn Ser Ser Ser Pro Ile Ser 225 230 235 240	720
gga gga gat cat gtg aaa ttg gct gca cca aac tgg gaa ttt cag aca Gly Gly Asp His Val Lys Leu Ala Ala Pro Asn Trp Glu Phe Gln Thr 245 250 255	768
aac aac aat acc tca aat ttc ttc gac aat ggc gga ttc tca tgg Asn Asn Asn Asn Thr Ser Asn Phe Asp Asn Gly Gly Phe Ser Trp 260 265 270	816
tct atc cca aat tct tct act tct tct tca caa gtc aaa cca aat cat Ser Ile Pro Asn Ser Ser Thr Ser Ser Gln Val Lys Pro Asn His 275 280 285	864
aac ttc gaa gaa ata aaa tgg tca gag tat ttg aac aca ccg ttc ttc Asn Phe Glu Glu Ile Lys Trp Ser Glu Tyr Leu Asn Thr Pro Phe Phe 290 295 300	912
ata ggg agt act gta cag agt caa acc tct caa cca atc tac atc aaa Ile Gly Ser Thr Val Gln Ser Gln Thr Ser Gln Pro Ile Tyr Ile Lys 305 310 315 320	960
tca gaa aca gat tac tta gcc aat gtt tca aac atg aca gat cct tgg Ser Glu Thr Asp Tyr Leu Ala Asn Val Ser Asn Met Thr Asp Pro Trp 325 330 335	1008
agc caa aac gag aac ttg ggc aca act gaa act agt gac gtg ttc tcc Ser Gln Asn Glu Asn Leu Gly Thr Glu Thr Ser Asp Val Phe Ser 340 345 350	1056
aag gat ctt cag aga atg gcc gtc tct ttt ggt cag tcc ctt tag Lys Asp Leu Gln Arg Met Ala Val Ser Phe Gly Gln Ser Leu 355 360 365	1101

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<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 26

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Met Gly Arg His Ser Cys Cys Tyr Lys Gln Lys Leu Arg Lys Gly Leu
1           5          10          15

Trp Ser Pro Glu Glu Asp Glu Lys Leu Leu Thr His Ile Thr Asn His
20          25          30

Gly His Gly Cys Trp Ser Ser Val Pro Lys Leu Ala Gly Leu Gln Arg
35          40          45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50          55          60

Leu Lys Arg Gly Ala Phe Ser Pro Glu Glu Asn Leu Ile Val Glu
65          70          75          80

Leu His Ala Val Leu Gly Asn Arg Trp Ser Gln Ile Ala Ser Arg Leu
85          90          95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Leu Trp Asn Ser Ser Ile
100         105         110

Lys Lys Lys Leu Lys Gln Arg Gly Ile Asp Pro Asn Thr His Lys Pro
115         120         125

Ile Ser Glu Val Glu Ser Phe Ser Asp Lys Asp Lys Pro Thr Thr Ser
130         135         140

Asn Asn Lys Arg Ser Gly Asn Asp His Lys Ser Pro Ser Ser Ser Ser
145         150         155         160

Ala Thr Asn Gln Asp Phe Phe Leu Glu Arg Pro Ser Asp Leu Ser Asp
165         170         175

Tyr Phe Gly Phe Gln Lys Leu Asn Phe Asn Ser Asn Leu Gly Leu Ser
180         185         190

Val Thr Thr Asp Ser Ser Leu Cys Ser Met Ile Pro Pro Gln Phe Ser
195         200         205

Pro Gly Asn Met Val Gly Ser Val Leu Gln Thr Pro Val Cys Val Lys
210         215         220

Pro Ser Ile Ser Leu Pro Pro Asp Asn Asn Ser Ser Ser Pro Ile Ser
225         230         235         240

Gly Gly Asp His Val Lys Leu Ala Ala Pro Asn Trp Glu Phe Gln Thr
245         250         255

Asn Asn Asn Thr Ser Asn Phe Phe Asp Asn Gly Gly Phe Ser Trp
260         265         270

Ser Ile Pro Asn Ser Ser Thr Ser Ser Ser Gln Val Lys Pro Asn His
275         280         285

Asn Phe Glu Glu Ile Lys Trp Ser Glu Tyr Leu Asn Thr Pro Phe Phe
290         295         300

Ile Gly Ser Thr Val Gln Ser Gln Thr Ser Gln Pro Ile Tyr Ile Lys
305         310         315         320

Ser Glu Thr Asp Tyr Leu Ala Asn Val Ser Asn Met Thr Asp Pro Trp
325         330         335

Ser Gln Asn Glu Asn Leu Gly Thr Thr Glu Thr Ser Asp Val Phe Ser
340         345         350

Lys Asp Leu Gln Arg Met Ala Val Ser Phe Gly Gln Ser Leu
355         360         365

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<210> SEQ ID NO 27

<211> LENGTH: 708

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

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<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1) .. (708)

<400> SEQUENCE: 27

atg gcc gat gag gtc aca atc ggg ttt cgc ttc tat ccc acg gaa gaa Met Ala Asp Glu Val Thr Ile Gly Phe Arg Phe Tyr Pro Thr Glu Glu	48
1 5 10 15	
gaa ctg gtt tcg ttc tac cta cga aac cag ctc gaa gga agg agt gat Glu Leu Val Ser Phe Tyr Leu Arg Asn Gln Leu Glu Gly Arg Ser Asp	96
20 25 30	
gac tca atg cat cgt gtc att ccc gta ctt gac gtc ttt gag gtc gag Asp Ser Met His Arg Val Ile Pro Val Leu Asp Val Phe Glu Val Glu	144
35 40 45	
cct agt cat ctt cca aat gtt gct gga gtg aga tgt cga gga gac gct Pro Ser His Leu Pro Asn Val Ala Gly Val Arg Cys Arg Gly Asp Ala	192
50 55 60	
gag caa tgg ttc ttc gtc gca caa gaa cgc gaa gca aga gga Glu Gln Trp Phe Phe Val Pro Arg Gln Glu Arg Glu Ala Arg Gly	240
65 70 75 80	
ggc aga ccg agt aga act act ggt tca gga tac tgg aaa gca act gga Gly Arg Pro Ser Arg Thr Thr Gly Ser Gly Tyr Trp Lys Ala Thr Gly	288
85 90 95	
tca cct ggt cca gtc ttt tcc aaa gac aac aaa atg att gga gca aag Ser Pro Gly Pro Val Phe Ser Lys Asp Asn Lys Met Ile Gly Ala Lys	336
100 105 110	
aaa act atg gtt ttc tac act gga aaa gca ccc aca gga aga aaa act Lys Thr Met Val Phe Tyr Thr Gly Lys Ala Pro Thr Gly Arg Lys Thr	384
115 120 125	
aaa tgg aaa atg aat gag tac cac gcc gtt gac gaa aca gtc aac gct Lys Trp Lys Met Asn Glu Tyr His Ala Val Asp Glu Thr Val Asn Ala	432
130 135 140	
tcc aca atc cct aag ctg aga cgt gag ttc agt tta tgt cga gtc tac Ser Thr Ile Pro Lys Leu Arg Arg Glu Phe Ser Leu Cys Arg Val Tyr	480
145 150 155 160	
ata aca aca gga agc tcc aga gct ttt gat aga cgt cct gag gga gtt Ile Thr Thr Gly Ser Ser Arg Ala Phe Asp Arg Arg Pro Glu Gly Val	528
165 170 175	
ttg cag aca gag aga atg cta aca agt gat gtt gca gta gct gag aca Leu Gln Thr Glu Arg Met Leu Thr Ser Asp Val Ala Val Ala Glu Thr	576
180 185 190	
tcg ttc cgt gtg gaa agc tca ctg gaa act tcg att tca gga gga gaa Ser Phe Arg Val Glu Ser Ser Leu Glu Thr Ser Ile Ser Gly Gly Glu	624
195 200 205	
cat att gat gtc tct atg aac aca gag ttt gtt gat gga cta tca gaa His Ile Asp Val Ser Met Asn Thr Glu Phe Val Asp Gly Leu Ser Glu	672
210 215 220	
ccg atg tgg gac tgg gaa cag ctg act tgg cct tga Pro Met Trp Asp Trp Glu Gln Leu Thr Trp Pro	708
225 230 235	

<210> SEQ ID NO 28

<211> LENGTH: 235

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 28

Met Ala Asp Glu Val Thr Ile Gly Phe Arg Phe Tyr Pro Thr Glu Glu 1 5 10 15	
Glu Leu Val Ser Phe Tyr Leu Arg Asn Gln Leu Glu Gly Arg Ser Asp 20 25 30	

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Asp Ser Met His Arg Val Ile Pro Val Leu Asp Val Phe Glu Val Glu
35 40 45

Pro Ser His Leu Pro Asn Val Ala Gly Val Arg Cys Arg Gly Asp Ala
50 55 60

Glu Gln Trp Phe Phe Val Pro Arg Gln Glu Arg Glu Ala Arg Gly
65 70 75 80

Gly Arg Pro Ser Arg Thr Thr Gly Ser Gly Tyr Trp Lys Ala Thr Gly
85 90 95

Ser Pro Gly Pro Val Phe Ser Lys Asp Asn Lys Met Ile Gly Ala Lys
100 105 110

Lys Thr Met Val Phe Tyr Thr Gly Lys Ala Pro Thr Gly Arg Lys Thr
115 120 125

Lys Trp Lys Met Asn Glu Tyr His Ala Val Asp Glu Thr Val Asn Ala
130 135 140

Ser Thr Ile Pro Lys Leu Arg Arg Glu Phe Ser Leu Cys Arg Val Tyr
145 150 155 160

Ile Thr Thr Gly Ser Ser Arg Ala Phe Asp Arg Arg Pro Glu Gly Val
165 170 175

Leu Gln Thr Glu Arg Met Leu Thr Ser Asp Val Ala Val Ala Glu Thr
180 185 190

Ser Phe Arg Val Glu Ser Ser Leu Glu Thr Ser Ile Ser Gly Gly Glu
195 200 205

His Ile Asp Val Ser Met Asn Thr Glu Phe Val Asp Gly Leu Ser Glu
210 215 220

Pro Met Trp Asp Trp Glu Gln Leu Thr Trp Pro
225 230 235

<210> SEQ ID NO 29
<211> LENGTH: 888
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(888)

<400> SEQUENCE: 29

atg gca aga caa atc aac ata gag agt agt gtt tct caa gtt acc ttt	48
Met Ala Arg Gln Ile Asn Ile Glu Ser Ser Val Ser Gln Val Thr Phe	
1 5 10 15	
atc tcc tcc gcc atc ccc gcc gta tct tcc tcc tcc atc acc acc gct	96
Ile Ser Ser Ala Ile Pro Ala Val Ser Ser Ser Ser Ile Thr Ala	
20 25 30	
tcc gcc tca ttg tcc tct tca cct act aca tct tcc tct tcg tca	144
Ser Ala Ser Leu Ser Ser Pro Thr Thr Ser Ser Ser Ser Ser Ser Ser	
35 40 45	
tca aca aat tct aac ttc att gag gaa gac aac tct aaa aga aaa gca	192
Ser Thr Asn Ser Asn Phe Ile Glu Asp Asn Ser Lys Arg Lys Ala	
50 55 60	
tct cga aga tca ttg tca tcg tta gtc tcc gtt gaa gac gat gat gat	240
Ser Arg Arg Ser Leu Ser Ser Leu Val Ser Val Glu Asp Asp Asp Asp	
65 70 75 80	
caa aac ggt gga ggt ggg aaa cgg cga aag acc aac ggt gga gat aaa	288
Gln Asn Gly Gly Gly Lys Arg Arg Lys Thr Asn Gly Gly Asp Lys	
85 90 95	
cat ccg acg tat aga gga gtg agg atg agg agt tgg gga aaa tgg gtg	336
His Pro Thr Tyr Arg Gly Val Arg Met Arg Ser Trp Gly Lys Trp Val	
100 105 110	

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tcg gag att aga gag ccg aga aag aaa tca aga atc tgg ctc ggg act Ser Glu Ile Arg Glu Pro Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr 115 120 125	384
tat cca acg gct gag atg gca gct cga gct cat gac gta gcg gct tta Tyr Pro Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu 130 135 140	432
gcc att aaa ggt aca acg gct tac ctc aat ttt ccc aag tta gcc ggc Ala Ile Lys Gly Thr Thr Ala Tyr Leu Asn Phe Pro Lys Leu Ala Gly 145 150 155 160	480
gag ctt cct cgt cca gtc aca aat tct cct aaa gac att caa gcc gcc Glu Leu Pro Arg Pro Val Thr Asn Ser Pro Lys Asp Ile Gln Ala Ala 165 170 175	528
gcc tct tta gcg gcc gtt aac tgg caa gat tcg gtc aac gat gtg agt Ala Ser Leu Ala Ala Val Asn Trp Gln Asp Ser Val Asn Asp Val Ser 180 185 190	576
aat tct gaa gtg gct gaa ata gtt gaa gcc gag ccg agt cga gcc gtg Asn Ser Glu Val Ala Glu Ile Val Glu Ala Glu Pro Ser Arg Ala Val 195 200 205	624
gtg gct cag ttg ttt tct tcg gac aca agc acg acg acg act cag Val Ala Gln Leu Phe Ser Ser Asp Thr Ser Thr Thr Thr Gln 210 215 220	672
agt caa gag tat tcg gaa gct tcg tgt gct tcg act tcg gcg tgt acg Ser Gln Glu Tyr Ser Glu Ala Ser Cys Ala Ser Thr Ser Ala Cys Thr 225 230 235 240	720
gac aaa gac agt gag gaa gag aag ctg ttt gat ttg ccg gat ttg ttt Asp Lys Asp Ser Glu Glu Glu Lys Leu Phe Asp Leu Pro Asp Leu Phe 245 250 255	768
acc gat gag aat gag atg atg ata cga aac gat gcg ttt tgc tac tac Thr Asp Glu Asn Glu Met Met Ile Arg Asn Asp Ala Phe Cys Tyr Tyr 260 265 270	816
tcg tcc acg tgg cag ctt tgt gga gcc gat gct ggg ttt cgg ctt gaa Ser Ser Thr Trp Gln Leu Cys Gly Ala Asp Ala Gly Phe Arg Leu Glu 275 280 285	864
gag ccg ttt ttt cta tct gaa tga Glu Pro Phe Phe Leu Ser Glu 290 295	888

<210> SEQ ID NO 30

<211> LENGTH: 295

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 30

Met Ala Arg Gln Ile Asn Ile Glu Ser Ser Val Ser Gln Val Thr Phe
1 5 10 15

Ile Ser Ser Ala Ile Pro Ala Val Ser Ser Ser Ser Ser Ile Thr Ala
20 25 30

Ser Ala Ser Leu Ser Ser Pro Thr Thr Ser Ser Ser Ser Ser Ser Ser
35 40 45

Ser Thr Asn Ser Asn Phe Ile Glu Glu Asp Asn Ser Lys Arg Lys Ala
50 55 60

Ser Arg Arg Ser Leu Ser Ser Leu Val Ser Val Glu Asp Asp Asp Asp
65 70 75 80

Gln Asn Gly Gly Gly Lys Arg Arg Lys Thr Asn Gly Gly Asp Lys
85 90 95

His Pro Thr Tyr Arg Gly Val Arg Met Arg Ser Trp Gly Lys Trp Val
100 105 110

Ser Glu Ile Arg Glu Pro Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr
115 120 125

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Tyr Pro Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu
 130 135 140

Ala Ile Lys Gly Thr Thr Ala Tyr Leu Asn Phe Pro Lys Leu Ala Gly
 145 150 155 160

Glu Leu Pro Arg Pro Val Thr Asn Ser Pro Lys Asp Ile Gln Ala Ala
 165 170 175

Ala Ser Leu Ala Ala Val Asn Trp Gln Asp Ser Val Asn Asp Val Ser
 180 185 190

Asn Ser Glu Val Ala Glu Ile Val Glu Ala Glu Pro Ser Arg Ala Val
 195 200 205

Val Ala Gln Leu Phe Ser Ser Asp Thr Ser Thr Thr Thr Thr Gln
 210 215 220

Ser Gln Glu Tyr Ser Glu Ala Ser Cys Ala Ser Thr Ser Ala Cys Thr
 225 230 235 240

Asp Lys Asp Ser Glu Glu Lys Leu Phe Asp Leu Pro Asp Leu Phe
 245 250 255

Thr Asp Glu Asn Glu Met Met Ile Arg Asn Asp Ala Phe Cys Tyr Tyr
 260 265 270

Ser Ser Thr Trp Gln Leu Cys Gly Ala Asp Ala Gly Phe Arg Leu Glu
 275 280 285

Glu Pro Phe Phe Leu Ser Glu
 290 295

<210> SEQ ID NO 31
 <211> LENGTH: 732
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(732)

<400> SEQUENCE: 31

atg gtc atg gag ccc aag aag aac caa aat cta cca agt ttc tta aac 1 5 10 15	48
Met Val Met Glu Pro Lys Lys Asn Gln Asn Leu Pro Ser Phe Leu Asn 20 25 30	96
cca tca cga cag aat cag gac aac gac aag aag agg aaa caa aca gag 35 40 45	144
gtt aaa ggt ttc gac att gtg gtc ggc gaa aag agg aag aag gag Val Lys Gly Phe Asp Ile Val Val Gly Glu Lys Arg Lys Lys Lys Glu 50 55 60	192
aat gaa gag gaa gac caa gaa att cag att ctt tat gag aag gag aag Asn Glu Glu Asp Gln Glu Ile Gln Ile Leu Tyr Glu Lys Glu Lys 65 70 75 80	240
aga gtt agg tta cct cca ctc tgt gca gca agg att tat caa ttg act Arg Val Arg Leu Pro Pro Leu Cys Ala Ala Arg Ile Tyr Gln Leu Thr 85 90 95	288
aaa gaa tta ggt cac aaa tca gat ggt gag act ctt gaa tgg ttg ctt Lys Glu Leu Gly His Lys Ser Asp Gly Glu Thr Leu Glu Trp Leu Leu 100 105 110	336
caa cat gct gag cca tcg ata ctc tct gct act gta aat ggt atc aaa Gln His Ala Glu Pro Ser Ile Leu Ser Ala Thr Val Asn Gly Ile Lys 115 120 125	384

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ccc act gag tct gtt gtt tct caa cct cct ctc acg gct gat ttg atg Pro Thr Glu Ser Val Val Ser Gln Pro Pro Leu Thr Ala Asp Leu Met 130 135 140	432
att tgt cat agc gtt gaa gaa gct tca agg act caa atg gag gca aat Ile Cys His Ser Val Glu Ala Ser Arg Thr Gln Met Glu Ala Asn 145 150 155 160	480
ggg ttg tgg aga aat gaa aca gga cag acc att gga ggg ttt gat ctg Gly Leu Trp Arg Asn Glu Thr Gly Gln Thr Ile Gly Gly Phe Asp Leu 165 170 175	528
aat tac gga att ggg ttt gat ttc aat ggt gtt cca gag att ggt ttt Asn Tyr Gly Ile Gly Phe Asp Phe Asn Gly Val Pro Glu Ile Gly Phe 180 185 190	576
gga gat aat caa acg cct gga ctt gaa tta agg ctg tct caa gtt ggg Gly Asp Asn Gln Thr Pro Gly Leu Glu Leu Arg Leu Ser Gln Val Gly 195 200 205	624
gtt ttg aat cca cag gtt ttt caa caa atg ggt aaa gaa cag ttc agg Val Leu Asn Pro Gln Val Phe Gln Gln Met Gly Lys Glu Gln Phe Arg 210 215 220	672
gtt ctt cat cat tca cat gaa gat cag cag cag agt gca gag gaa Val Leu His His Ser His Glu Asp Gln Gln Ser Ala Glu Glu 225 230 235 240	720
aat ggt tca taa Asn Gly Ser	732

<210> SEQ ID NO 32
<211> LENGTH: 243
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 32

Met Val Met Glu Pro Lys Lys Asn Gln Asn Leu Pro Ser Phe Leu Asn 1 5 10 15
Pro Ser Arg Gln Asn Gln Asp Asn Asp Lys Lys Arg Lys Gln Thr Glu 20 25 30
Val Lys Gly Phe Asp Ile Val Val Gly Glu Lys Arg Lys Lys Lys Glu 35 40 45
Asn Glu Glu Asp Gln Glu Ile Gln Ile Leu Tyr Glu Lys Glu Lys 50 55 60
Lys Lys Pro Asn Lys Asp Arg His Leu Lys Val Glu Gly Arg Gly Arg 65 70 75 80
Arg Val Arg Leu Pro Pro Leu Cys Ala Ala Arg Ile Tyr Gln Leu Thr 85 90 95
Lys Glu Leu Gly His Lys Ser Asp Gly Glu Thr Leu Glu Trp Leu Leu 100 105 110
Gln His Ala Glu Pro Ser Ile Leu Ser Ala Thr Val Asn Gly Ile Lys 115 120 125
Pro Thr Glu Ser Val Val Ser Gln Pro Pro Leu Thr Ala Asp Leu Met 130 135 140
Ile Cys His Ser Val Glu Glu Ala Ser Arg Thr Gln Met Glu Ala Asn 145 150 155 160
Gly Leu Trp Arg Asn Glu Thr Gly Gln Thr Ile Gly Gly Phe Asp Leu 165 170 175
Asn Tyr Gly Ile Gly Phe Asp Phe Asn Gly Val Pro Glu Ile Gly Phe 180 185 190
Gly Asp Asn Gln Thr Pro Gly Leu Glu Leu Arg Leu Ser Gln Val Gly 195 200 205

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Val Leu Asn Pro Gln Val Phe Gln Gln Met Gly Lys Glu Gln Phe Arg
210 215 220

Val Leu His His His Ser His Glu Asp Gln Gln Gln Ser Ala Glu Glu
225 230 235 240

Asn Gly Ser

<210> SEQ ID NO 33
<211> LENGTH: 1083
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(1083)

<400> SEQUENCE: 33

atg aga tca gga gaa tgt gat gaa gag gag att caa gca aag caa gaa Met Arg Ser Gly Glu Cys Asp Glu Glu Glu Ile Gln Ala Lys Gln Glu 1 5 10 15	48
aga gat caa aat caa aat cat caa gta aac tta aac cac atg ttg caa Arg Asp Gln Asn Gln Asn His Gln Val Asn Leu Asn His Met Leu Gln 20 25 30	96
caa caa cag ccg agt tcg gta tca tct tca agg caa tgg act tca gct Gln Gln Gln Pro Ser Ser Val Ser Ser Arg Gln Trp Thr Ser Ala 35 40 45	144
ttt agg aat cca aga atc gtt cga gtc tca aga aca ttc ggt ggc aaa Phe Arg Asn Pro Arg Ile Val Arg Val Ser Arg Thr Phe Gly Gly Lys 50 55 60	192
gac aga cac agc aaa gta tgt aca gtc cgt ggt ctt cga gac ccg agg Asp Arg His Ser Lys Val Cys Thr Val Arg Gly Leu Arg Asp Arg Arg 65 70 75 80	240
ata agg ttg tcc gta cct aca gct att caa ctc tac gac ctt caa gat Ile Arg Leu Ser Val Pro Thr Ala Ile Gln Leu Tyr Asp Leu Gln Asp 85 90 95	288
cga tta ggg ctg agt cag cca agc aaa gtc att gat tgg tta ctc gaa Arg Leu Gly Leu Ser Gln Pro Ser Lys Val Ile Asp Trp Leu Leu Glu 100 105 110	336
gca gca aaa gat gac gta gac aag cta cct cct cta caa ttc cca cat Ala Ala Lys Asp Asp Val Asp Lys Leu Pro Pro Leu Gln Phe Pro His 115 120 125	384
gga ttt aac cag atg tat cca aat ctc atc ttc gga aac tcc ggg ttt Gly Phe Asn Gln Met Tyr Pro Asn Leu Ile Phe Gly Asn Ser Gly Phe 130 135 140	432
gga gaa tct cca tct tca act aca tca aca acg ttt cca gga acc aat Gly Glu Ser Pro Ser Ser Thr Thr Ser Thr Thr Phe Pro Gly Thr Asn 145 150 155 160	480
ctc ggg ttc ttg gaa aat tgg gat ctt ggt ggt tct tca aga aca aga Leu Gly Phe Leu Glu Asn Trp Asp Leu Gly Gly Ser Ser Arg Thr Arg 165 170 175	528
gca aga tta acc gat aca act acg acc caa aga gaa agt ttt gat ctt Ala Arg Leu Thr Asp Thr Thr Thr Gln Arg Glu Ser Phe Asp Leu 180 185 190	576
gat aaa gga aaa tgg atc aaa aac gac gag aat agt aat caa gat cat Asp Lys Gly Lys Trp Ile Lys Asn Asp Glu Asn Ser Asn Gln Asp His 195 200 205	624
caa ggg ttt aac acc aat cat caa caa ttt cct ctg acc aat ccg Gln Gly Phe Asn Thr Asn His Gln Gln Gln Phe Pro Leu Thr Asn Pro 210 215 220	672
tac aac aac act tca gct tat tac aac ctt gga cat ctt caa caa tcg Tyr Asn Asn Thr Ser Ala Tyr Tyr Asn Leu Gly His Leu Gln Gln Ser 225 230 235 240	720

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108

tta gac caa tct ggt aat aac gtt act gtc gca ata tct aat gtt gct Leu Asp Gln Ser Gly Asn Asn Val Thr Val Ala Ile Ser Asn Val Ala 245 250 255	768
gct aat aat aac aat aat ctc aat ttg cat cct cct tcc tcg tct gcc Ala Asn Asn Asn Asn Leu Asn Leu His Pro Pro Ser Ser Ala 260 265 270	816
gga gat gga tct cag ctt ttc ggt cct act cct ccg gca atg agc Gly Asp Gly Ser Gln Leu Phe Gly Pro Thr Pro Pro Ala Met Ser 275 280 285	864
tct cta ttc ccg aca tac cct tcg ttt ctt gga gct tct cat cat cat Ser Leu Phe Pro Thr Tyr Pro Ser Phe Leu Gly Ala Ser His His His 290 295 300	912
cat gtc gtc gat gga gcc ggt cat ctt cag ctc ttt agc tcg aat tca His Val Val Asp Gly Ala Gly His Leu Gln Leu Phe Ser Ser Asn Ser 305 310 315 320	960
aat acc gca tcg cag caa cac atg atg ccg ggt aat acg agt ttg att Asn Thr Ala Ser Gln Gln His Met Met Pro Gly Asn Thr Ser Leu Ile 325 330 335	1008
aga cca ttt cat cat ttg atg agc tcg aat cat gat acg gat cat cat Arg Pro Phe His His Leu Met Ser Ser Asn His Asp Thr Asp His His 340 345 350	1056
agt agc gat aat gaa tca gat tct tga Ser Ser Asp Asn Glu Ser Asp Ser 355 360	1083

<210> SEQ ID NO 34

<211> LENGTH: 360

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 34

Met Arg Ser Gly Glu Cys Asp Glu Glu Glu Ile Gln Ala Lys Gln Glu 1 5 10 15
Arg Asp Gln Asn Gln Asn His Gln Val Asn Leu Asn His Met Leu Gln 20 25 30
Gln Gln Gln Pro Ser Ser Val Ser Ser Arg Gln Trp Thr Ser Ala 35 40 45
Phe Arg Asn Pro Arg Ile Val Arg Val Ser Arg Thr Phe Gly Gly Lys 50 55 60
Asp Arg His Ser Lys Val Cys Thr Val Arg Gly Leu Arg Asp Arg Arg 65 70 75 80
Ile Arg Leu Ser Val Pro Thr Ala Ile Gln Leu Tyr Asp Leu Gln Asp 85 90 95
Arg Leu Gly Leu Ser Gln Pro Ser Lys Val Ile Asp Trp Leu Leu Glu 100 105 110
Ala Ala Lys Asp Asp Val Asp Lys Leu Pro Pro Leu Gln Phe Pro His 115 120 125
Gly Phe Asn Gln Met Tyr Pro Asn Leu Ile Phe Gly Asn Ser Gly Phe 130 135 140
Gly Glu Ser Pro Ser Ser Thr Thr Ser Thr Thr Phe Pro Gly Thr Asn 145 150 155 160
Leu Gly Phe Leu Glu Asn Trp Asp Leu Gly Gly Ser Ser Arg Thr Arg 165 170 175
Ala Arg Leu Thr Asp Thr Thr Thr Gln Arg Glu Ser Phe Asp Leu 180 185 190
Asp Lys Gly Lys Trp Ile Lys Asn Asp Glu Asn Ser Asn Gln Asp His 195 200 205

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Gln Gly Phe Asn Thr Asn His Gln Gln Phe Pro Leu Thr Asn Pro
210 215 220

Tyr Asn Asn Thr Ser Ala Tyr Tyr Asn Leu Gly His Leu Gln Gln Ser
225 230 235 240

Leu Asp Gln Ser Gly Asn Asn Val Thr Val Ala Ile Ser Asn Val Ala
245 250 255

Ala Asn Asn Asn Asn Leu Asn Leu His Pro Pro Ser Ser Ala
260 265 270

Gly Asp Gly Ser Gln Leu Phe Phe Gly Pro Thr Pro Pro Ala Met Ser
275 280 285

Ser Leu Phe Pro Thr Tyr Pro Ser Phe Leu Gly Ala Ser His His His
290 295 300

His Val Val Asp Gly Ala Gly His Leu Gln Leu Phe Ser Ser Asn Ser
305 310 315 320

Asn Thr Ala Ser Gln Gln His Met Met Pro Gly Asn Thr Ser Leu Ile
325 330 335

Arg Pro Phe His His Leu Met Ser Ser Asn His Asp Thr Asp His His
340 345 350

Ser Ser Asp Asn Glu Ser Asp Ser
355 360

<210> SEQ_ID NO 35
<211> LENGTH: 777
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(777)

<400> SEQUENCE: 35

atg gga aag aga gca act act agt gtg agg aga gaa gag tta aac aga	48
Met Gly Lys Arg Ala Thr Thr Ser Val Arg Arg Glu Glu Leu Asn Arg	
1 5 10 15	
gga gct tgg act gat cat gaa gac aag atc ctt aga gat tac atc acc	96
Gly Ala Trp Thr Asp His Glu Asp Lys Ile Leu Arg Asp Tyr Ile Thr	
20 25 30	
act cac ggc gaa ggc aaa tgg agc act ctc cct aac caa gct ggt ctc	144
Thr His Gly Glu Gly Lys Trp Ser Thr Leu Pro Asn Gln Ala Gly Leu	
35 40 45	
aag agg tgt ggc aaa agc tgt aga ctt cgg tgg aag aac tac cta aga	192
Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Lys Asn Tyr Leu Arg	
50 55 60	
ccg ggg ata aag cgc ggt aac atc tca tct gat gaa gaa gaa ctc ata	240
Pro Gly Ile Lys Arg Gly Asn Ile Ser Ser Asp Glu Glu Glu Leu Ile	
65 70 75 80	
atc cgt ctc cat aat ctt ctt gga aac aga tgg tcg ttg ata gct ggg	288
Ile Arg Leu His Asn Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly	
85 90 95	
agg ctt cca ggc cga aca gac aat gaa ata aag aat cat tgg aac tca	336
Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn His Trp Asn Ser	
100 105 110	
aac ctc cgc aaa aga ctt ccc aaa act caa acc aag caa cca aaa cgt	384
Asn Leu Arg Lys Arg Leu Pro Lys Thr Gln Thr Lys Gln Pro Lys Arg	
115 120 125	
ata aaa cat tcg acg aac aac gag aat aat gta tgt gtt ata cgt aca	432
Ile Lys His Ser Thr Asn Asn Glu Asn Asn Val Cys Val Ile Arg Thr	
130 135 140	

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aag gcg att agg tgc tca aag act ctt ctc ttc tcg gat ctc tct ctt Lys Ala Ile Arg Cys Ser Lys Thr Leu Leu Phe Ser Asp Leu Ser Leu 145 150 155 160	480
cag aag aag agt act agt cca cta cct ctg aaa gaa caa gag atg Gln Lys Lys Ser Ser Thr Ser Pro Leu Pro Leu Lys Glu Gln Glu Met 165 170 175	528
gat caa ggt gga tct tcg ttg atg gga gat ctc gaa ttc gat ttc gat Asp Gln Gly Gly Ser Ser Leu Met Gly Asp Leu Glu Phe Asp Phe Asp 180 185 190	576
agg atc cat tcg gag ttt cac ttc ccg gat ttg atg gat ttt gat ggt Arg Ile His Ser Glu Phe His Phe Pro Asp Leu Met Asp Phe Asp Gly 195 200 205	624
ttg gac tgt gga aac gtt aca tct ctt gtt tca tct aac gag att ttg Leu Asp Cys Gly Asn Val Thr Ser Leu Val Ser Ser Asn Glu Ile Leu 210 215 220	672
gga gag ttg cct gct caa ggt aat ctc gat ctc aat aga cct ttc Gly Glu Leu Val Pro Ala Gln Gly Asn Leu Asp Leu Asn Arg Pro Phe 225 230 235 240	720
act tct tgt cat cat cgt ggc gac gat gaa gat tgg ctc cga gac ttc Thr Ser Cys His His Arg Gly Asp Asp Glu Asp Trp Leu Arg Asp Phe 245 250 255	768
act tgt tga Thr Cys	777

<210> SEQ ID NO: 36

<211> LENGTH: 258

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 36

Met Gly Lys Arg Ala Thr Thr Ser Val Arg Arg Glu Glu Leu Asn Arg 1 5 10 15
--

Gly Ala Trp Thr Asp His Glu Asp Lys Ile Leu Arg Asp Tyr Ile Thr 20 25 30

Thr His Gly Glu Gly Lys Trp Ser Thr Leu Pro Asn Gln Ala Gly Leu 35 40 45

Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Lys Asn Tyr Leu Arg 50 55 60

Pro Gly Ile Lys Arg Gly Asn Ile Ser Ser Asp Glu Glu Glu Leu Ile 65 70 75 80
--

Ile Arg Leu His Asn Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly 85 90 95

Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn His Trp Asn Ser 100 105 110
--

Asn Leu Arg Lys Arg Leu Pro Lys Thr Gln Thr Lys Gln Pro Lys Arg 115 120 125
--

Ile Lys His Ser Thr Asn Asn Glu Asn Asn Val Cys Val Ile Arg Thr 130 135 140
--

Lys Ala Ile Arg Cys Ser Lys Thr Leu Leu Phe Ser Asp Leu Ser Leu 145 150 155 160
--

Gln Lys Lys Ser Ser Thr Ser Pro Leu Pro Leu Lys Glu Gln Glu Met 165 170 175
--

Asp Gln Gly Gly Ser Ser Leu Met Gly Asp Leu Glu Phe Asp Phe Asp 180 185 190
--

Arg Ile His Ser Glu Phe His Phe Pro Asp Leu Met Asp Phe Asp Gly 195 200 205
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Leu Asp Cys Gly Asn Val Thr Ser Leu Val Ser Ser Asn Glu Ile Leu
210 215 220

Gly Glu Leu Val Pro Ala Gln Gly Asn Leu Asp Leu Asn Arg Pro Phe
225 230 235 240

Thr Ser Cys His His Arg Gly Asp Asp Glu Asp Trp Leu Arg Asp Phe
245 250 255

Thr Cys

<210> SEQ ID NO 37

<211> LENGTH: 528

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1) .. (528)

<400> SEQUENCE: 37

atg atg aag tca aga cgt gaa caa tca atc gaa gaa gca atc gtc gca	48
Met Met Lys Ser Arg Arg Glu Gln Ser Ile Glu Glu Ala Ile Val Ala	
1 5 10 15	

aat tat ttg aag atg atg atc gat aac gta aac gtt tgg cct cgc cac	96
Asn Tyr Leu Lys Met Met Ile Asp Asn Val Asn Val Trp Pro Arg His	
20 25 30	

ttc ctc cga agc gaa gac gtg tac tgc aag aat ccg tgg acg ctt ttc	144
Phe Leu Arg Ser Glu Asp Val Tyr Cys Lys Asn Pro Trp Thr Leu Phe	
35 40 45	

gtt act aga gat cct ata atc cta cac ttc gga cga tac ttc ttc gtt	192
Val Thr Arg Asp Pro Ile Ile Leu His Phe Gly Arg Tyr Phe Phe Val	
50 55 60	

aat cgg agt gtg aat tca ggt tta acc gat gga tgt gaa tac ggt tgt	240
Asn Arg Ser Val Asn Ser Gly Leu Thr Asp Gly Cys Glu Tyr Gly Cys	
65 70 75 80	

tgg aga atc atc ggt cgt gat aga gtg atc aag tcg gtg acg acc ggg	288
Trp Arg Ile Ile Gly Arg Asp Arg Val Ile Lys Ser Val Thr Thr Gly	
85 90 95	

aag att cta ggg tta aag aag gtt tat aag ttc tgt gaa act gat cgg	336
Lys Ile Leu Gly Leu Lys Val Tyr Lys Phe Cys Glu Thr Asp Arg	
100 105 110	

aaa ccg aaa tcg gtt ttt aag ttc ttg gaa aag gag aag aga aga gta	384
Lys Pro Lys Ser Val Phe Lys Phe Leu Glu Lys Glu Lys Arg Arg Val	
115 120 125	

aga gat aga cga atc tgg gcg atg gaa gag tat agg ttt gca agt acg	432
Arg Asp Arg Arg Ile Trp Ala Met Glu Glu Tyr Arg Phe Ala Ser Thr	
130 135 140	

tgg aaa caa gat tac gtg atc tgc aag att cga cgt ctg tat cca caa	480
Trp Lys Gln Asp Tyr Val Ile Cys Lys Ile Arg Arg Leu Tyr Pro Gln	
145 150 155 160	

cca ttt gac tac atg ttg gcc cag cac att cga ggt tac tat aaa tga	528
Pro Phe Asp Tyr Met Leu Ala Gln His Ile Arg Gly Tyr Tyr Lys	
165 170 175	

<210> SEQ ID NO 38
<211> LENGTH: 175
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 38

Met Met Lys Ser Arg Arg Glu Gln Ser Ile Glu Glu Ala Ile Val Ala	
1 5 10 15	

Asn Tyr Leu Lys Met Met Ile Asp Asn Val Asn Val Trp Pro Arg His	
20 25 30	

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Phe Leu Arg Ser Glu Asp Val Tyr Cys Lys Asn Pro Trp Thr Leu Phe
 35 40 45

Val Thr Arg Asp Pro Ile Ile Leu His Phe Gly Arg Tyr Phe Phe Val
 50 55 60

Asn Arg Ser Val Asn Ser Gly Leu Thr Asp Gly Cys Glu Tyr Gly Cys
 65 70 75 80

Trp Arg Ile Ile Gly Arg Asp Arg Val Ile Lys Ser Val Thr Thr Gly
 85 90 95

Lys Ile Leu Gly Leu Lys Lys Val Tyr Lys Phe Cys Glu Thr Asp Arg
 100 105 110

Lys Pro Lys Ser Val Phe Lys Phe Leu Glu Lys Glu Lys Arg Arg Val
 115 120 125

Arg Asp Arg Arg Ile Trp Ala Met Glu Glu Tyr Arg Phe Ala Ser Thr
 130 135 140

Trp Lys Gln Asp Tyr Val Ile Cys Lys Ile Arg Arg Leu Tyr Pro Gln
 145 150 155 160

Pro Phe Asp Tyr Met Leu Ala Gln His Ile Arg Gly Tyr Tyr Lys
 165 170 175

<210> SEQ_ID NO 39
 <211> LENGTH: 930
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1) .. (930)

<400> SEQUENCE: 39

atg tct ggt tcg acc cgg aaa gaa atg gat cgg atc aaa gga cca tgg Met Ser Gly Ser Thr Arg Lys Glu Met Asp Arg Ile Lys Gly Pro Trp 1 5 10 15	48
agt cct gaa gaa gac gat ctg tta caa tcg ttg gtt cag aag cac gga Ser Pro Glu Glu Asp Asp Leu Leu Gln Ser Leu Val Gln Lys His Gly 20 25 30	96
cca agg aac tgg tct ctg ata agc aaa tca atc cct gga cgt tcc ggt Pro Arg Asn Trp Ser Leu Ile Ser Lys Ser Ile Pro Gly Arg Ser Gly 35 40 45	144
aaa tct tgc cgt ctc cgt tgg tgt aat cag ctt tct ccg gag gta gag Lys Ser Cys Arg Leu Arg Trp Cys Asn Gln Leu Ser Pro Glu Val Glu 50 55 60	192
cac cgt gga ttc acg gcg gag gaa gat gat acg att ata cta gcg cac His Arg Gly Phe Thr Ala Glu Glu Asp Asp Thr Ile Ile Leu Ala His 65 70 75 80	240
gct cgg ttt ggt aac aag tgg gcg acg att gca cgg ctt ctc aat ggt Ala Arg Phe Gly Asn Lys Trp Ala Thr Ile Ala Arg Leu Leu Asn Gly 85 90 95	288
cgc act gat aac gcg att aag aat cac tgg aac tca acg ctg aag cgg Arg Thr Asp Asn Ala Ile Lys Asn His Trp Asn Ser Thr Leu Lys Arg 100 105 110	336
aaa tgt agc ggc gga ggc ggc gga gag gaa ggg cag agt tgt gat Lys Cys Ser Gly Gly Gly Gly Glu Glu Gly Gln Ser Cys Asp 115 120 125	384
ttc ggt ggt aat gga ggg tat gat ggt aat tta act gat gaa aaa ccg Phe Gly Gly Asn Gly Gly Tyr Asp Gly Asn Leu Thr Asp Glu Lys Pro 130 135 140	432
tta aaa cgg agg gcg agt ggt gga gga gtt gtt gtg gtg acg gcg Leu Lys Arg Arg Ala Ser Gly Gly Val Val Val Val Thr Ala 145 150 155 160	480

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Leu Ser Pro Thr Gly Ser Asp Val Ser Glu Gln Ser Gln Ser Ser Gly
 165 170 175
 Ser Val Leu Pro Val Ser Ser Ser Cys His Val Phe Lys Pro Thr Ala
 180 185 190
 Arg Ala Gly Gly Val Val Ile Glu Ser Ser Ser Pro Glu Glu Glu
 195 200 205
 Lys Asp Pro Met Thr Cys Leu Arg Leu Ser Leu Pro Trp Val Asn Glu
 210 215 220
 Ser Thr Thr Pro Pro Glu Leu Phe Pro Val Lys Arg Glu Glu Glu
 225 230 235 240
 Glu Lys Glu Arg Glu Ile Ser Gly Leu Gly Gly Asp Phe Met Thr Val
 245 250 255
 Val Gln Glu Met Ile Lys Thr Glu Val Arg Ser Tyr Met Ala Asp Leu
 260 265 270
 Gln Leu Gly Asn Gly Gly Ala Gly Gly Ala Ser Ser Cys Met
 275 280 285
 Val Gln Gly Thr Asn Gly Arg Asn Val Gly Phe Arg Glu Phe Ile Gly
 290 295 300
 Leu Gly Arg Ile Glu
 305

<210> SEQ_ID NO 41
 <211> LENGTH: 621
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(621)

<400> SEQUENCE: 41

atg gag gtg gag aag agg att gta gtg aat gga gga atg aaa ttg cca	48
Met Glu Val Glu Lys Arg Ile Val Val Asn Gly Gly Met Lys Leu Pro	
1 5 10 15	
ata gga tac aga ttt cac cca acc gag caa gag ctt atc ctt cat tac	96
Ile Gly Tyr Arg Phe His Pro Thr Glu Gln Glu Leu Ile Leu His Tyr	
20 25 30	
ttt ctc cca aag gcc ttt gct tct cct ttg cct tcc atc atc cct	144
Leu Leu Pro Lys Ala Phe Ala Ser Pro Leu Pro Ser Ser Ile Ile Pro	
35 40 45	
gtc ttt gac ctc ttc ttc tct cat cct ctt agt ttc cca ggg gac caa	192
Val Phe Asp Leu Phe Phe Ser His Pro Leu Ser Phe Pro Gly Asp Gln	
50 55 60	
aag gag aag cag agg tac ttc ttt tgc aag aag aga gaa gtg tca agt	240
Lys Glu Lys Gln Arg Tyr Phe Phe Cys Lys Lys Arg Glu Val Ser Ser	
65 70 75 80	
aat gag cat aga atc aag att tcc tct ggt gat ggt tat tgg aaa cct	288
Asn Glu His Arg Ile Lys Ile Ser Ser Gly Asp Gly Tyr Trp Lys Pro	
85 90 95	
att ggt aaa gag aga cca atc att gcc tct ggt aaa aca ttt ggg att	336
Ile Gly Lys Glu Arg Pro Ile Ile Ala Cys Gly Lys Thr Phe Gly Ile	
100 105 110	
aga aga aca ctt gct ttc tat gaa aca aac aag tct tct tat tgc	384
Arg Arg Thr Leu Ala Phe Tyr Glu Thr Asn Lys Ser Ser Ser Tyr Cys	
115 120 125	
aac aaa act aga tgg agc atg aca gag tat tgt ctt gcg gga ttt gcg	432
Asn Lys Thr Arg Trp Ser Met Thr Glu Tyr Cys Leu Ala Gly Phe Ala	
130 135 140	

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tcg gct aag gtg tct gga gaa tgg gca gtc tac aat gtt tat gag agg	480
Ser Ala Lys Val Ser Gly Glu Trp Ala Val Tyr Asn Val Tyr Glu Arg	
145 150 155 160	
aaa ggc tca aaa gga aga aaa cag agg aaa tca aga gag gga gat gat	528
Lys Gly Ser Lys Gly Arg Lys Gln Arg Lys Ser Arg Glu Gly Asp Asp	
165 170 175	
gaa gaa ttg aga tgc atc gac cat ttt acg gtt ggg tca aat cat gaa	576
Glu Glu Leu Arg Cys Ile Asp His Phe Thr Val Gly Ser Asn His Glu	
180 185 190	
acc ggt cca cca ccg cct tct cct acc tca gct gat gag taa	621
Thr Gly Pro Pro Pro Pro Ser Pro Pro Thr Ser Ala Asp Glu	
195 200 205	

<210> SEQ ID NO 42
<211> LENGTH: 206
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 42

Met Glu Val Glu Lys Arg Ile Val Val Asn Gly Gly Met Lys Leu Pro	
1 5 10 15	
Ile Gly Tyr Arg Phe His Pro Thr Glu Gln Glu Leu Ile Leu His Tyr	
20 25 30	
Leu Leu Pro Lys Ala Phe Ala Ser Pro Leu Pro Ser Ser Ile Ile Pro	
35 40 45	
Val Phe Asp Leu Phe Phe Ser His Pro Leu Ser Phe Pro Gly Asp Gln	
50 55 60	
Lys Glu Lys Gln Arg Tyr Phe Phe Cys Lys Lys Arg Glu Val Ser Ser	
65 70 75 80	
Asn Glu His Arg Ile Lys Ile Ser Ser Gly Asp Gly Tyr Trp Lys Pro	
85 90 95	
Ile Gly Lys Glu Arg Pro Ile Ile Ala Cys Gly Lys Thr Phe Gly Ile	
100 105 110	
Arg Arg Thr Leu Ala Phe Tyr Glu Thr Asn Lys Ser Ser Ser Tyr Cys	
115 120 125	
Asn Lys Thr Arg Trp Ser Met Thr Glu Tyr Cys Leu Ala Gly Phe Ala	
130 135 140	
Ser Ala Lys Val Ser Gly Glu Trp Ala Val Tyr Asn Val Tyr Glu Arg	
145 150 155 160	
Lys Gly Ser Lys Gly Arg Lys Gln Arg Lys Ser Arg Glu Gly Asp Asp	
165 170 175	
Glu Glu Leu Arg Cys Ile Asp His Phe Thr Val Gly Ser Asn His Glu	
180 185 190	
Thr Gly Pro Pro Pro Pro Ser Pro Pro Thr Ser Ala Asp Glu	
195 200 205	

<210> SEQ ID NO 43
<211> LENGTH: 1416
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1) .. (1416)

<400> SEQUENCE: 43

atg gag ttg gag cct ata tca tcg agt tgt tgc tcg tcg tct tct tct	48
Met Glu Leu Glu Pro Ile Ser Ser Ser Cys Cys Ser Ser Ser Ser Ser	
1 5 10 15	

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tct tct ggg gag gag aat act gcg gcg gcg aac atg acg gag atg gag Ser Ser Gly Glu Glu Asn Thr Ala Ala Ala Asn Met Thr Glu Met Glu 20 25 30	96
gcg gca gaa gca ttg gcg gat tta gcg cag ctt gcg ata atg cga gag Ala Ala Glu Ala Leu Ala Asp Leu Ala Gln Leu Ala Ile Met Arg Glu 35 40 45	144
cag gtt ttc gaa tct gca gcg agt tgg gga agt aaa ggg aaa cgg gtg Gln Val Phe Glu Ser Ala Ala Ser Trp Gly Ser Lys Gly Lys Arg Val 50 55 60	192
agg aag cga gtc aag act gag tct cct tct gac tcg ctt ttg aaa Arg Lys Arg Val Lys Thr Glu Ser Pro Pro Ser Asp Ser Leu Leu Lys 65 70 75 80	240
cca cct gac tct gat acg tta cct act ccg gat cta gct gag gaa cga Pro Pro Asp Ser Asp Thr Leu Pro Thr Pro Asp Leu Ala Glu Glu Arg 85 90 95	288
tta gtg aaa gaa gaa gag gaa gaa gaa gtt gaa cca ata act aaa Leu Val Lys Glu Glu Glu Glu Glu Val Glu Pro Ile Thr Lys 100 105 110	336
gaa cta act aaa gct ccg gtt aaa tct gaa atc aat ggt gaa aca cct Glu Leu Thr Lys Ala Pro Val Lys Ser Glu Ile Asn Gly Glu Thr Pro 115 120 125	384
aaa cca att ctt gct tcg act cta ata agg tgt agt aga tca aat ggt Lys Pro Ile Leu Ala Ser Thr Leu Ile Arg Cys Ser Arg Ser Asn Gly 130 135 140	432
tgt ggc cga tca aga cag aat tta agt gag gct gaa aga gaa cgt Cys Gly Arg Ser Arg Gln Asn Leu Ser Glu Arg Glu Glu Arg 145 150 155 160	480
aga atc aga agg ata tta gct aat aga gaa tct gcg agg cag aca att Arg Ile Arg Arg Ile Leu Ala Asn Arg Glu Ser Ala Arg Gln Thr Ile 165 170 175	528
cgg cga aga cag gca atg tgt gag gag ttg agt aaa aaa gca gct gat Arg Arg Arg Gln Ala Met Cys Glu Leu Ser Lys Lys Ala Ala Asp 180 185 190	576
ctg aca tat gag aat gag aat ttg agg agg gaa aag gat tgg gct ttg Leu Thr Tyr Glu Asn Glu Asn Leu Arg Arg Glu Lys Asp Trp Ala Leu 195 200 205	624
aaa gag ttt cag tct ttg gag acg att aac aag cat tta aag gaa cag Lys Glu Phe Gln Ser Leu Glu Thr Ile Asn Lys His Leu Lys Glu Gln 210 215 220	672
gta ttg aag tca gta aaa ccc gat aca aaa gag cct gaa gaa tca ccc Val Leu Lys Ser Val Lys Pro Asp Thr Lys Glu Pro Glu Glu Ser Pro 225 230 235 240	720
aag cca tca caa gtt gag atg tct aca tca tct act ccg ttt tac ttc Lys Pro Ser Gln Val Glu Met Ser Thr Ser Ser Thr Pro Phe Tyr Phe 245 250 255	768
tac aac cag aat cca tat cag ctt ttc tgc tgg cct cat gtt act caa Tyr Asn Gln Asn Pro Tyr Gln Leu Phe Cys Trp Pro His Val Thr Gln 260 265 270	816
tca tca aat cca atg ata tcg cca ctt gaa ttc cct act tcg gga gga Ser Ser Asn Pro Met Ile Ser Pro Leu Glu Phe Pro Thr Ser Gly Gly 275 280 285	864
gct tct gct aaa act att acc acg cag gag cat gaa aat gct gca gat Ala Ser Ala Lys Thr Ile Thr Thr Gln Glu His Glu Asn Ala Ala Asp 290 295 300	912
gat aat ggg caa aaa act cac ttt tac gtt gta cct tgc cct tgg ttt Asp Asn Gly Gln Lys Thr His Phe Tyr Val Val Pro Cys Pro Trp Phe 305 310 315 320	960
ctc cct cct gat cac agc aat ggt gtt cct ttc ggg ctt caa gat Leu Pro Pro Asp His Ser Asn Gly Val Pro Phe Gly Leu Gln Asp 325 330 335	1008

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aca caa aga ggt act ttt tca aac ggg cac cat atc gat gat tct tct	1056
Thr Gln Arg Gly Thr Phe Ser Asn Gly His His Ile Asp Asp Ser Ser	
340 345 350	
gca aga ccg atg gat gtc aca gaa act ccg cgg tcc cat cta cca act	1104
Ala Arg Pro Met Asp Val Thr Glu Thr Pro Arg Ser His Leu Pro Thr	
355 360 365	
aga atc aaa gaa gag gac tct ggt tca ccc gaa acc aga cct tta tat	1152
Arg Ile Lys Glu Glu Asp Ser Gly Ser Pro Glu Thr Arg Pro Leu Tyr	
370 375 380	
gat ctc aac gaa tct gct act gaa gtc ctc tca gaa gga gga gat gga	1200
Asp Leu Asn Glu Ser Ala Thr Glu Val Leu Ser Glu Gly Gly Asp Gly	
385 390 395 400	
ttt cct gta acg cag caa gct tat agt tta aag cat gaa gat gtt tct	1248
Phe Pro Val Thr Gln Gln Ala Tyr Ser Leu Lys His Glu Asp Val Ser	
405 410 415	
gag aca act aat gga gtt aca ctg atg ccg cct ggt cat cat gtt ttg	1296
Glu Thr Thr Asn Gly Val Thr Leu Met Pro Pro Gly His His Val Leu	
420 425 430	
att tct cta ccg gag aaa aag cat gga tcg ttg gct gca gcg gaa gct	1344
Ile Ser Leu Pro Glu Lys Lys Gly Ser Leu Ala Ala Ala Glu Ala	
435 440 445	
aga aag aga cgg aaa gaa ctc aca agg ctc aag aac ctc cat ggc cgt	1392
Arg Lys Arg Arg Lys Glu Leu Thr Arg Leu Lys Asn Leu His Gly Arg	
450 455 460	
caa tgt ccg atg cag gtc gga taa	1416
Gln Cys Arg Met Gln Val Gly	
465 470	

<210> SEQ ID NO 44
<211> LENGTH: 471
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 44

Met Glu Leu Glu Pro Ile Ser Ser Ser Cys Cys Ser Ser Ser Ser Ser	
1 5 10 15	
Ser Ser Gly Glu Glu Asn Thr Ala Ala Ala Asn Met Thr Glu Met Glu	
20 25 30	
Ala Ala Glu Ala Leu Ala Asp Leu Ala Gln Leu Ala Ile Met Arg Glu	
35 40 45	
Gln Val Phe Glu Ser Ala Ala Ser Trp Gly Ser Lys Gly Lys Arg Val	
50 55 60	
Arg Lys Arg Val Lys Thr Glu Ser Pro Pro Ser Asp Ser Leu Leu Lys	
65 70 75 80	
Pro Pro Asp Ser Asp Thr Leu Pro Thr Pro Asp Leu Ala Glu Glu Arg	
85 90 95	
Leu Val Lys Glu Glu Glu Glu Glu Val Glu Pro Ile Thr Lys	
100 105 110	
Glu Leu Thr Lys Ala Pro Val Lys Ser Glu Ile Asn Gly Glu Thr Pro	
115 120 125	
Lys Pro Ile Leu Ala Ser Thr Leu Ile Arg Cys Ser Arg Ser Asn Gly	
130 135 140	
Cys Gly Arg Ser Arg Gln Asn Leu Ser Glu Ala Glu Arg Glu Glu Arg	
145 150 155 160	
Arg Ile Arg Arg Ile Leu Ala Asn Arg Glu Ser Ala Arg Gln Thr Ile	
165 170 175	

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Arg Arg Arg Gln Ala Met Cys Glu Glu Leu Ser Lys Lys Ala Ala Asp
180 185 190

Leu Thr Tyr Glu Asn Glu Asn Leu Arg Arg Glu Lys Asp Trp Ala Leu
195 200 205

Lys Glu Phe Gln Ser Leu Glu Thr Ile Asn Lys His Leu Lys Glu Gln
210 215 220

Val Leu Lys Ser Val Lys Pro Asp Thr Lys Glu Pro Glu Glu Ser Pro
225 230 235 240

Lys Pro Ser Gln Val Glu Met Ser Thr Ser Ser Thr Pro Phe Tyr Phe
245 250 255

Tyr Asn Gln Asn Pro Tyr Gln Leu Phe Cys Trp Pro His Val Thr Gln
260 265 270

Ser Ser Asn Pro Met Ile Ser Pro Leu Glu Phe Pro Thr Ser Gly Gly
275 280 285

Ala Ser Ala Lys Thr Ile Thr Thr Gln Glu His Glu Asn Ala Ala Asp
290 295 300

Asp Asn Gly Gln Lys Thr His Phe Tyr Val Val Pro Cys Pro Trp Phe
305 310 315 320

Leu Pro Pro Pro Asp His Ser Asn Gly Val Pro Phe Gly Leu Gln Asp
325 330 335

Thr Gln Arg Gly Thr Phe Ser Asn Gly His His Ile Asp Asp Ser Ser
340 345 350

Ala Arg Pro Met Asp Val Thr Glu Thr Pro Arg Ser His Leu Pro Thr
355 360 365

Arg Ile Lys Glu Glu Asp Ser Gly Ser Pro Glu Thr Arg Pro Leu Tyr
370 375 380

Asp Leu Asn Glu Ser Ala Thr Glu Val Leu Ser Glu Gly Asp Gly
385 390 395 400

Phe Pro Val Thr Gln Gln Ala Tyr Ser Leu Lys His Glu Asp Val Ser
405 410 415

Glu Thr Thr Asn Gly Val Thr Leu Met Pro Pro Gly His His Val Leu
420 425 430

Ile Ser Leu Pro Glu Lys Lys His Gly Ser Leu Ala Ala Ala Glu Ala
435 440 445

Arg Lys Arg Arg Lys Glu Leu Thr Arg Leu Lys Asn Leu His Gly Arg
450 455 460

Gln Cys Arg Met Gln Val Gly
465 470

<210> SEQ ID NO 45
<211> LENGTH: 1077
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1077)

<400> SEQUENCE: 45

atg gct gat aat aag gtc aat ctt tcg att aat gga caa tca aaa gtg	48
Met Ala Asp Asn Lys Val Asn Leu Ser Ile Asn Gly Gln Ser Lys Val	
1 5 10 15	
cct cca ggt ttc aga ttc cat ccc acc gaa gaa ctt ctc cat tac	96
Pro Pro Gly Phe Arg Phe His Pro Thr Glu Glu Leu Leu His Tyr	
20 25 30	
tat ctc cgt aag aaa gtt aac tct caa aag atc gat ctt gat gtc att	
Tyr Leu Arg Lys Lys Val Asn Ser Gln Lys Ile Asp Leu Asp Val Ile	
35 40 45	

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cgt gaa gtt gat cta aac aag ctt gag cct tgg gat att caa gag gaa Arg Glu Val Asp Leu Asn Lys Leu Glu Pro Trp Asp Ile Gln Glu Glu 50 55 60	192
tgt aga atc ggt tca acg cca caa aac gac tgg tac ttc ttc agc cac Cys Arg Ile Gly Ser Thr Pro Gln Asn Asp Trp Tyr Phe Phe Ser His 65 70 75 80	240
aag gac aag aag tat cca acc ggg acc agg acg aac cgg gca aca gtc Lys Asp Lys Lys Tyr Pro Thr Gly Thr Arg Thr Asn Arg Ala Thr Val 85 90 95	288
gct gga ttc tgg aaa gct acc gga cgt gac aaa atc atc tgc agt tgt Ala Gly Phe Trp Lys Ala Thr Gly Arg Asp Lys Ile Ile Cys Ser Cys 100 105 110	336
gtc cgg aga att gga ctg agg aag aca ctc gtg ttc tac aaa gga aga Val Arg Arg Ile Gly Leu Arg Lys Thr Leu Val Phe Tyr Lys Gly Arg 115 120 125	384
get cct cac ggt cag aaa tcc gac tgg atc atg cat gag tat cgc ctc Ala Pro His Gly Gln Lys Ser Asp Trp Ile Met His Glu Tyr Arg Leu 130 135 140	432
gac gat act cca atg tct aat ggc tat gct gat gtt gtt aca gaa gat Asp Asp Thr Pro Met Ser Asn Gly Tyr Ala Asp Val Val Thr Glu Asp 145 150 155 160	480
cca atg agc tat aac gaa gaa ggt tgg gtg gta tgt cga gtg ttc agg Pro Met Ser Tyr Asn Glu Glu Gly Trp Val Val Cys Arg Val Phe Arg 165 170 175	528
aag aag aac tat caa aag att gac gat tgt cct aaa atc act cta tct Lys Lys Asn Tyr Gln Lys Ile Asp Asp Cys Pro Lys Ile Thr Leu Ser 180 185 190	576
tct tta cct gat gac acg gag gaa gag aag ggg ccc acc ttt cac aac Ser Leu Pro Asp Asp Thr Glu Glu Lys Gly Pro Thr Phe His Asn 195 200 205	624
act caa aac gtt acc ggt tta gac cat gtt ctt ctc tac atg gac cgt Thr Gln Asn Val Thr Gly Leu Asp His Val Leu Leu Tyr Met Asp Arg 210 215 220	672
acc ggt tct aac att tgc atg ccc gag agc caa aca acg act caa cat Thr Gly Ser Asn Ile Cys Met Pro Glu Ser Gln Thr Thr Gln His 225 230 235 240	720
caa gat gat gtc tta ttc atg caa ctc cca agt ctt gag aca cct aaa Gln Asp Asp Val Leu Phe Met Gln Leu Pro Ser Leu Glu Thr Pro Lys 245 250 255	768
tcc gag agc ccg gtc gac caa agt ttc ctg act cca agc aaa ctc gat Ser Glu Ser Pro Val Asp Gln Ser Phe Leu Thr Pro Ser Lys Leu Asp 260 265 270	816
ttc tct ccc gtt caa gag aag ata acc gaa aga ccg gtt tgc agc aac Phe Ser Pro Val Gln Glu Lys Ile Thr Glu Arg Pro Val Cys Ser Asn 275 280 285	864
tgg gct agt ctt gac ccg ctc gta gct tgg caa ttg aac aat ggt cat Trp Ala Ser Leu Asp Arg Leu Val Ala Trp Gln Leu Asn Asn Gly His 290 295 300	912
cat aat ccg tgt cat cgt aag agt ttt gat gaa gaa gaa aat ggt His Asn Pro Cys His Arg Lys Ser Phe Asp Glu Glu Glu Asn Gly 305 310 315 320	960
gat act atg atg cag cga tgg gat ctt cat tgg aat aat gat gat aat Asp Thr Met Met Gln Arg Trp Asp Leu His Trp Asn Asn Asp Asp Asn 325 330 335	1008
gtt gat ctt tgg agt agt ttc act gag tct tct tcg tct tta gac cca Val Asp Leu Trp Ser Ser Phe Thr Glu Ser Ser Ser Ser Leu Asp Pro 340 345 350	1056

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ctt ctt cat tta tct gta tga
 Leu Leu His Leu Ser Val
 355

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<210> SEQ ID NO 46
 <211> LENGTH: 358
 <212> TYPE: PRT
 <213> ORGANISM: Arabidopsis thaliana
 <400> SEQUENCE: 46

Met Ala Asp Asn Lys Val Asn Leu Ser Ile Asn Gly Gln Ser Lys Val			
1	5	10	15
Pro Pro Gly Phe Arg Phe His Pro Thr Glu Glu Glu Leu Leu His Tyr			
20	25	30	
Tyr Leu Arg Lys Lys Val Asn Ser Gln Lys Ile Asp Leu Asp Val Ile			
35	40	45	
Arg Glu Val Asp Leu Asn Lys Leu Glu Pro Trp Asp Ile Gln Glu Glu			
50	55	60	
Cys Arg Ile Gly Ser Thr Pro Gln Asn Asp Trp Tyr Phe Phe Ser His			
65	70	75	80
Lys Asp Lys Lys Tyr Pro Thr Gly Thr Arg Thr Asn Arg Ala Thr Val			
85	90	95	
Ala Gly Phe Trp Lys Ala Thr Gly Arg Asp Lys Ile Ile Cys Ser Cys			
100	105	110	
Val Arg Arg Ile Gly Leu Arg Lys Thr Leu Val Phe Tyr Lys Gly Arg			
115	120	125	
Ala Pro His Gly Gln Lys Ser Asp Trp Ile Met His Glu Tyr Arg Leu			
130	135	140	
Asp Asp Thr Pro Met Ser Asn Gly Tyr Ala Asp Val Val Thr Glu Asp			
145	150	155	160
Pro Met Ser Tyr Asn Glu Glu Gly Trp Val Val Cys Arg Val Phe Arg			
165	170	175	
Lys Lys Asn Tyr Gln Lys Ile Asp Asp Cys Pro Lys Ile Thr Leu Ser			
180	185	190	
Ser Leu Pro Asp Asp Thr Glu Glu Lys Gly Pro Thr Phe His Asn			
195	200	205	
Thr Gln Asn Val Thr Gly Leu Asp His Val Leu Leu Tyr Met Asp Arg			
210	215	220	
Thr Gly Ser Asn Ile Cys Met Pro Glu Ser Gln Thr Thr Gln His			
225	230	235	240
Gln Asp Asp Val Leu Phe Met Gln Leu Pro Ser Leu Glu Thr Pro Lys			
245	250	255	
Ser Glu Ser Pro Val Asp Gln Ser Phe Leu Thr Pro Ser Lys Leu Asp			
260	265	270	
Phe Ser Pro Val Gln Glu Lys Ile Thr Glu Arg Pro Val Cys Ser Asn			
275	280	285	
Trp Ala Ser Leu Asp Arg Leu Val Ala Trp Gln Leu Asn Asn Gly His			
290	295	300	
His Asn Pro Cys His Arg Lys Ser Phe Asp Glu Glu Glu Asn Gly			
305	310	315	320
Asp Thr Met Met Gln Arg Trp Asp Leu His Trp Asn Asn Asp Asn Asn			
325	330	335	
Val Asp Leu Trp Ser Ser Phe Thr Glu Ser Ser Ser Leu Asp Pro			
340	345	350	

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Leu Leu His Leu Ser Val
355

<210> SEQ ID NO 47
<211> LENGTH: 732
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(732)

<400> SEQUENCE: 47

atg tac gga cag tgc aat ata gaa tcc gac tac gct ttg ttg gag tcg	48
Met Tyr Gly Gln Cys Asn Ile Glu Ser Asp Tyr Ala Leu Leu Glu Ser	
1 5 10 15	
ata aca cgt cac ttg cta gga gga gga gag aac gag ctg cga ctc	96
Ile Thr Arg His Leu Leu Gly Gly Gly Glu Asn Glu Leu Arg Leu	
20 25 30	
aat gag tca aca ccg agt tcg tgt ttc aca gag agt tgg gga ggt ttg	144
Asn Glu Ser Thr Pro Ser Ser Cys Phe Thr Glu Ser Trp Gly Gly Leu	
35 40 45	
cca ttg aaa gag aat gat tca gag gac atg ttg gtg tac gga ctc ctc	192
Pro Leu Lys Glu Asn Asp Ser Glu Asp Met Leu Val Tyr Gly Leu Leu	
50 55 60	
aaa gat gcc ttc cat ttt gac acg tca tca tcg gac ttg agc tgt ctt	240
Lys Asp Ala Phe His Phe Asp Thr Ser Ser Asp Leu Ser Cys Leu	
65 70 75 80	
ttt gat ttt ccg gcg gtt aaa gtc gag cca act gag aac ttt acg gcg	288
Phe Asp Phe Pro Ala Val Lys Val Glu Pro Thr Glu Asn Phe Thr Ala	
85 90 95	
atg gag gag aaa cca aag aaa gcg ata ccg gtt acg gag acg gca gtg	336
Met Glu Glu Lys Pro Lys Lys Ala Ile Pro Val Thr Glu Thr Ala Val	
100 105 110	
aag gcg aag cat tac aga gga gtg agg cag aga ccg tgg ggg aaa ttc	384
Lys Ala Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe	
115 120 125	
gcg gcg gag ata cgt gat ccg gcg aag aat gga gct agg gtt tgg tta	432
Ala Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu	
130 135 140	
ggg acg ttt gag acg gcg gaa gat gcg gct tta gct tac gat ata gct	480
Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Ile Ala	
145 150 155 160	
gct ttt agg atg cgt ggt tcc cgc gct tta ttg aat ttt ccg ttg agg	528
Ala Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg	
165 170 175	
gtt aat tcc ggt gaa cct gac ccg gtt cggt atc acg tct aag aga tct	576
Val Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Thr Ser Lys Arg Ser	
180 185 190	
tct tcg tcg tcg tcg tcg tcc tct tct acg tcg tcg tct gaa aac	624
Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Glu Asn	
195 200 205	
ggg aag ttg aaa cga agg aga aaa gca gag aat ctg acg tcg gag gtg	672
Gly Lys Leu Lys Arg Arg Arg Lys Ala Glu Asn Leu Thr Ser Glu Val	
210 215 220	
gtg cag gtg aag tgt gag ggt gat gag aca cgt gtt gat gag tta	720
Val Gln Val Lys Cys Glu Val Gly Asp Glu Thr Arg Val Asp Glu Leu	
225 230 235 240	
ttg gtt tca taa	732
Leu Val Ser	

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<210> SEQ ID NO 48
<211> LENGTH: 243
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana
<400> SEQUENCE: 48

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Met Tyr Gly Gln Cys Asn Ile Glu Ser Asp Tyr Ala Leu Leu Glu Ser
1           5          10          15

Ile Thr Arg His Leu Leu Gly Gly Gly Glu Asn Glu Leu Arg Leu
20          25          30

Asn Glu Ser Thr Pro Ser Ser Cys Phe Thr Glu Ser Trp Gly Gly Leu
35          40          45

Pro Leu Lys Glu Asn Asp Ser Glu Asp Met Leu Val Tyr Gly Leu Leu
50          55          60

Lys Asp Ala Phe His Phe Asp Thr Ser Ser Asp Leu Ser Cys Leu
65          70          75          80

Phe Asp Phe Pro Ala Val Lys Val Glu Pro Thr Glu Asn Phe Thr Ala
85          90          95

Met Glu Glu Lys Pro Lys Lys Ala Ile Pro Val Thr Glu Thr Ala Val
100         105         110

Lys Ala Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe
115         120         125

Ala Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu
130         135         140

Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Ile Ala
145         150         155         160

Ala Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg
165         170         175

Val Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Thr Ser Lys Arg Ser
180         185         190

Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Glu Asn
195         200         205

Gly Lys Leu Lys Arg Arg Arg Lys Ala Glu Asn Leu Thr Ser Glu Val
210         215         220

Val Gln Val Lys Cys Glu Val Gly Asp Glu Thr Arg Val Asp Glu Leu
225         230         235         240

Leu Val Ser

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<210> SEQ ID NO 49
<211> LENGTH: 747
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(747)
<400> SEQUENCE: 49

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atg gag ggt tcg tcc aaa ggg ctg cga aaa ggt gct tgg act act gaa      48
Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Thr Glu
1           5          10          15

gaa gat agt ctc ttg aga cag tgc att aat aag tat gga gaa ggc aaa      96
Glu Asp Ser Leu Leu Arg Gln Cys Ile Asn Lys Tyr Gly Glu Gly Lys
20          25          30

tgg cac caa gtt cct gta aga gct ggg cta aac cgg tgc agg aaa agt
Trp His Gln Val Pro Val Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
35          40          45

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tgt aga tta aga tgg ttg aac tat ttg aag cca agt atc aag aga gga Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly 50 55 60	192
aaa ctt agc tct gat gaa gtc gat ctt ctt cgc ctt cat agg ctt Lys Leu Ser Ser Asp Glu Val Asp Leu Leu Arg Leu His Arg Leu 65 70 75 80	240
cta ggg aat agg tgg tct tta att gct gga aga tta cct ggt cgg acc Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr 85 90 95	288
gca aat gag gtc aag aat tac tgg aac act cat ctg agt aag aaa cat Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His 100 105 110	336
gaa ccg tgt aag ata aag atg aaa aag aga gac att acg ccc att Glu Pro Cys Cys Lys Ile Lys Met Lys Lys Arg Asp Ile Thr Pro Ile 115 120 125	384
cct aca aca ccg gca cta aaa aac aat gtt tat aag cct cga cct cga Pro Thr Thr Pro Ala Leu Lys Asn Asn Val Tyr Lys Pro Arg Pro Arg 130 135 140	432
tcc ttc aca gtt aac aac gac tgc aac cat ctc aat gcc cca cca aaa Ser Phe Thr Val Asn Asn Asp Cys Asn His Leu Asn Ala Pro Pro Lys 145 150 155 160	480
gtt gac gtt aat cct cca tgc ctt gga ctt aac atc aat aat gtt tgt Val Asp Val Asn Pro Pro Cys Leu Gly Leu Asn Ile Asn Asn Val Cys 165 170 175	528
gac aat agt atc ata tac aac aaa gat aag aag aaa gac caa cta gtg Asp Asn Ser Ile Ile Tyr Asn Lys Asp Lys Lys Asp Gln Leu Val 180 185 190	576
aat aat ttg att gat gga gat aat atg tgg tta gag aaa ttc cta gag Asn Asn Leu Ile Asp Gly Asp Asn Met Trp Leu Glu Lys Phe Leu Glu 195 200 205	624
gaa agc caa gag gta gat att ttg gtt cct gaa gcg acg aca aca gaa Glu Ser Gln Glu Val Asp Ile Leu Val Pro Glu Ala Thr Thr Glu 210 215 220	672
aag ggg gac acc ttg gct ttt gac gtt gat caa ctt tgg agt ctt ttc Lys Gly Asp Thr Leu Ala Phe Asp Val Asp Gln Leu Trp Ser Leu Phe 225 230 235 240	720
gat gga gag act gtg aaa ttt gat tag Asp Gly Glu Thr Val Lys Phe Asp 245	747

<210> SEQ ID NO 50
<211> LENGTH: 248
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 50

Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Thr Glu 1 5 10 15
Glu Asp Ser Leu Leu Arg Gln Cys Ile Asn Lys Tyr Gly Glu Gly Lys 20 25 30
Trp His Gln Val Pro Val Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser 35 40 45
Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly 50 55 60
Lys Leu Ser Ser Asp Glu Val Asp Leu Leu Arg Leu His Arg Leu 65 70 75 80
Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr 85 90 95

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Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
100 105 110

Glu Pro Cys Cys Lys Ile Lys Met Lys Lys Arg Asp Ile Thr Pro Ile
115 120 125

Pro Thr Thr Pro Ala Leu Lys Asn Asn Val Tyr Lys Pro Arg Pro Arg
130 135 140

Ser Phe Thr Val Asn Asn Asp Cys Asn His Leu Asn Ala Pro Pro Lys
145 150 155 160

Val Asp Val Asn Pro Pro Cys Leu Gly Leu Asn Ile Asn Asn Val Cys
165 170 175

Asp Asn Ser Ile Ile Tyr Asn Lys Asp Lys Lys Lys Asp Gln Leu Val
180 185 190

Asn Asn Leu Ile Asp Gly Asp Asn Met Trp Leu Glu Lys Phe Leu Glu
195 200 205

Glu Ser Gln Glu Val Asp Ile Leu Val Pro Glu Ala Thr Thr Thr Glu
210 215 220

Lys Gly Asp Thr Leu Ala Phe Asp Val Asp Gln Leu Trp Ser Leu Phe
225 230 235 240

Asp Gly Glu Thr Val Lys Phe Asp
245

<210> SEQ_ID NO 51
<211> LENGTH: 1113
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(1113)

<400> SEQUENCE: 51

atg ggt cat cac tca tgc tgc aac cag caa aag gtg aag aga ggg ctt	48
Met Gly His His Ser Cys Cys Asn Gln Gln Lys Val Lys Arg Gly Leu	
1 5 10 15	
tgg tca ccg gaa gaa gat gag aag ctt att aga tat atc aca act cat	96
Trp Ser Pro Glu Glu Asp Glu Lys Leu Ile Arg Tyr Ile Thr Thr His	
20 25 30	
ggc tat gga tgt tgg agt gaa gtc cct gaa aaa gca ggg ctt caa aga	144
Gly Tyr Gly Cys Trp Ser Glu Val Pro Glu Lys Ala Gly Leu Gln Arg	
35 40 45	
tgt gga aaa agt tgt aga ttg cga tgg ata aac tat ctt cga cct gat	192
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp	
50 55 60	
atc agg aga gga agg ttc tct cca gaa gaa gag aaa ttg atc ata agc	240
Ile Arg Arg Gly Arg Phe Ser Pro Glu Glu Lys Leu Ile Ile Ser	
65 70 75 80	
ctt cat gga gtt gtg gga aac agg tgg gct cat ata gct agt cat tta	288
Leu His Gly Val Val Gly Asn Arg Trp Ala His Ile Ala Ser His Leu	
85 90 95	
ccg gga aga aca gat aac gag att aaa aac tat tgg aat tca tgg att	336
Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser Trp Ile	
100 105 110	
aag aaa aag ata cga aaa ccg cac cat tac agt cgt cat caa ccg	384
Lys Lys Ile Arg Lys Pro His His His Tyr Ser Arg His Gln Pro	
115 120 125	
tca gta act act gtg aca ttg aat gcg gac act aca tcg att gcc act	432
Ser Val Thr Thr Val Thr Leu Asn Ala Asp Thr Thr Ser Ile Ala Thr	
130 135 140	

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acc atc gag gcc tct acc acc aca aca tcg act atc gat aac tta cat	480
Thr Ile Glu Ala Ser Thr Thr Thr Ser Thr Ile Asp Asn Leu His	
145 150 155 160	
ttt gac ggt ttc act gat tct cct aac caa tta aat ttc acc aat gat	528
Phe Asp Gly Phe Thr Asp Ser Pro Asn Gln Leu Asn Phe Thr Asn Asp	
165 170 175	
caa gaa act aat ata aag att caa gaa act ttt ttc tcc cat aaa cct	576
Gln Glu Thr Asn Ile Lys Ile Gln Glu Thr Phe Phe Ser His Lys Pro	
180 185 190	
cct ctc ttc atg gta gac aca aca ctt cct atc cta gaa gga atg ttc	624
Pro Leu Phe Met Val Asp Thr Thr Leu Pro Ile Leu Glu Gly Met Phe	
195 200 205	
tct gaa aac atc atc aca aac aat aac aag aac aat gat cat gat gac	672
Ser Glu Asn Ile Ile Thr Asn Asn Lys Asn Asn His Asp Asp	
210 215 220	
acg caa aga gga gga aca aat gtt tgt gaa caa gca ttt cta aca	720
Thr Gln Arg Gly Gly Glu Asn Val Cys Glu Gln Ala Phe Leu Thr	
225 230 235 240	
act aac acg gaa gaa tgg gat atg aat ctt cgt cag caa gag ccg ttt	768
Thr Asn Thr Glu Glu Trp Asp Met Asn Leu Arg Gln Gln Glu Pro Phe	
245 250 255	
caa gtt cct aca ctg gcg tca cat gtg ttc aac aac tct tcc aat tca	816
Gln Val Pro Thr Leu Ala Ser His Val Phe Asn Asn Ser Ser Asn Ser	
260 265 270	
aat att gac acg gtt ata agt tat aat cta ccg gcg cta ata gag gga	864
Asn Ile Asp Thr Val Ile Ser Tyr Asn Leu Pro Ala Leu Ile Glu Gly	
275 280 285	
aat gtc gat aac atc gtc cat aat gaa aac agc aat gtc caa gat gga	912
Asn Val Asp Asn Ile Val His Asn Glu Asn Ser Asn Val Gln Asp Gly	
290 295 300	
gaa atg gcg tcc aca ttc gaa tgt tta aag agg caa gaa cta agc tat	960
Glu Met Ala Ser Thr Phe Glu Cys Leu Lys Arg Gln Glu Leu Ser Tyr	
305 310 315 320	
gat caa tgg gac gat tca caa caa tgc tct aac ttt ttc ttt tgg gac	1008
Asp Gln Trp Asp Asp Ser Gln Gln Cys Ser Asn Phe Phe Trp Asp	
325 330 335	
aac ctt aat ata aac gtg gaa ggt tca tct ctt gtt gga aac caa gac	1056
Asn Leu Asn Ile Asn Val Glu Gly Ser Ser Leu Val Gly Asn Gln Asp	
340 345 350	
cca tca atg aat ttg gga tca tct gcc tta tct tct ttc cct tct	1104
Pro Ser Met Asn Leu Gly Ser Ser Ala Leu Ser Ser Phe Pro Ser	
355 360 365	
tcg ttt taa	1113
Ser Phe	
370	

<210> SEQ ID NO: 52

<211> LENGTH: 370

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 52

Met Gly His His Ser Cys Cys Asn Gln Gln Lys Val Lys Arg Gly Leu	
1 5 10 15	

Trp Ser Pro Glu Glu Asp Glu Lys Leu Ile Arg Tyr Ile Thr Thr His	
20 25 30	

Gly Tyr Gly Cys Trp Ser Glu Val Pro Glu Lys Ala Gly Leu Gln Arg	
35 40 45	

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp	
50 55 60	

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Ile Arg Arg Gly Arg Phe Ser Pro Glu Glu Glu Lys Leu Ile Ile Ser
65 70 75 80

Leu His Gly Val Val Gly Asn Arg Trp Ala His Ile Ala Ser His Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser Trp Ile
100 105 110

Lys Lys Lys Ile Arg Lys Pro His His His Tyr Ser Arg His Gln Pro
115 120 125

Ser Val Thr Thr Val Thr Leu Asn Ala Asp Thr Thr Ser Ile Ala Thr
130 135 140

Thr Ile Glu Ala Ser Thr Thr Thr Ser Thr Ile Asp Asn Leu His
145 150 155 160

Phe Asp Gly Phe Thr Asp Ser Pro Asn Gln Leu Asn Phe Thr Asn Asp
165 170 175

Gln Glu Thr Asn Ile Lys Ile Gln Glu Thr Phe Phe Ser His Lys Pro
180 185 190

Pro Leu Phe Met Val Asp Thr Thr Leu Pro Ile Leu Glu Gly Met Phe
195 200 205

Ser Glu Asn Ile Ile Thr Asn Asn Asn Lys Asn Asn Asp His Asp Asp
210 215 220

Thr Gln Arg Gly Arg Glu Asn Val Cys Glu Gln Ala Phe Leu Thr
225 230 235 240

Thr Asn Thr Glu Glu Trp Asp Met Asn Leu Arg Gln Gln Glu Pro Phe
245 250 255

Gln Val Pro Thr Leu Ala Ser His Val Phe Asn Asn Ser Ser Asn Ser
260 265 270

Asn Ile Asp Thr Val Ile Ser Tyr Asn Leu Pro Ala Leu Ile Glu Gly
275 280 285

Asn Val Asp Asn Ile Val His Asn Glu Asn Ser Asn Val Gln Asp Gly
290 295 300

Glu Met Ala Ser Thr Phe Glu Cys Leu Lys Arg Gln Glu Leu Ser Tyr
305 310 315 320

Asp Gln Trp Asp Asp Ser Gln Gln Cys Ser Asn Phe Phe Trp Asp
325 330 335

Asn Leu Asn Ile Asn Val Glu Gly Ser Ser Leu Val Gly Asn Gln Asp
340 345 350

Pro Ser Met Asn Leu Gly Ser Ser Ala Leu Ser Ser Ser Phe Pro Ser
355 360 365

Ser Phe
370

<210> SEQ ID NO 53
<211> LENGTH: 1095
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1095)

<400> SEQUENCE: 53

atg gag acc gat tct tcc ggt ggt cca cca ccg cca caa cct aac	48
Met Glu Ser Thr Asp Ser Ser Gly Gly Pro Pro Pro Pro Gln Pro Asn	
1 5 10 15	
ctt cct cca ggc ttc cgg ttt cac cct acc gac gaa gag ctt gtt gtt	96
Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Val Val	
20 25 30	

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cac tac ctc aaa cgc aaa gca gcc tct gct cct tta cct gtc gcc atc His Tyr Leu Lys Arg Lys Ala Ala Ser Ala Pro Leu Pro Val Ala Ile 35 40 45	144
atc gcc gaa gtc gat ctc tat aaa ttt gat cca tgg gaa ctt ccc gct Ile Ala Glu Val Asp Leu Tyr Lys Phe Asp Pro Trp Glu Leu Pro Ala 50 55 60	192
aaa gca tcg ttt gga gaa caa gaa tgg tac ttc ttt agt cca cga gat Lys Ala Ser Phe Gly Glu Gln Glu Trp Tyr Phe Ser Pro Arg Asp 65 70 75 80	240
cgg aag tat cca aac gga gca aga cca aac aga gcg gcg act tca ggt Arg Lys Tyr Pro Asn Gly Ala Arg Pro Asn Arg Ala Ala Thr Ser Gly 85 90 95	288
tat tgg aaa gcg acc ggt aca gat aaa ccg gta ctt gct tcc gac ggt Tyr Trp Lys Ala Thr Gly Thr Asp Lys Pro Val Leu Ala Ser Asp Gly 100 105 110	336
aac caa aag gtg ggc gtg aag aag gca cta gtc ttc tac agt ggt aaa Asn Gln Lys Val Gly Val Lys Lys Ala Leu Val Phe Tyr Ser Gly Lys 115 120 125	384
cca cca aaa ggc gtt aaa agt gat tgg atc atg cat gag tat cgt ctc Pro Pro Lys Gly Val Lys Ser Asp Trp Ile Met His Glu Tyr Arg Leu 130 135 140	432
atc gaa aac aaa cca aac aat cga cct cct ggc tgg ttt ggc aac Ile Glu Asn Lys Pro Asn Asn Arg Pro Pro Gly Cys Asp Phe Gly Asn 145 150 155 160	480
aaa aaa aac tca ctc aga ctt gat gat tgg gtg tta tgt aga atc tac Lys Lys Asn Ser Leu Arg Leu Asp Asp Trp Val Leu Cys Arg Ile Tyr 165 170 175	528
aag aag aac aac gca agt cga cat gtt gat aac gat aag gat cat gat Lys Lys Asn Asn Ala Ser Arg His Val Asp Asn Asp Lys Asp His Asp 180 185 190	576
atg atc gat tac att ttc agg aag att cct ccg tct tta tca atg gcg Met Ile Asp Tyr Ile Phe Arg Lys Ile Pro Pro Ser Leu Ser Met Ala 195 200 205	624
gct gct tct aca gga ctt cac caa cat cat cat aat gtc tca aga tca Ala Ala Ser Thr Gly Leu His Gln His His His Asn Val Ser Arg Ser 210 215 220	672
atg aat ttc ttc cct ggc aaa ttc tcc ggt ggt ggt tac ggg att ttc Met Asn Phe Pro Gly Lys Phe Ser Gly Gly Tyr Gly Ile Phe 225 230 235 240	720
tct gac ggt ggt aac acg agt ata tac gac ggc ggt ggc atg atc aac Ser Asp Gly Gly Asn Thr Ser Ile Tyr Asp Gly Gly Met Ile Asn 245 250 255	768
aat att ggt act gac tca gta gat cac gac aat aac gct gac gtc gtt Asn Ile Gly Thr Asp Ser Val Asp His Asp Asn Asn Ala Asp Val Val 260 265 270	816
ggt tta aat cat gct tcg tcg tca ggt cct atg atg atg gcg aat ttg Gly Leu Asn His Ala Ser Ser Ser Gly Pro Met Met Met Ala Asn Leu 275 280 285	864
aaa cga act ctc ccg gtg ccg tat tgg cct gta gca gat gag gag caa Lys Arg Thr Leu Pro Val Pro Tyr Trp Pro Val Ala Asp Glu Glu Gln 290 295 300	912
gat gca tct ccg agc aaa cgg ttt cac ggt gta gga gga gga gga Asp Ala Ser Pro Ser Lys Arg Phe His Gly Val Gly Gly Gly Gly 305 310 315 320	960
gat tgt tcg aac atg tct tcc atg atg gaa gag gag act cca cca ttg Asp Cys Ser Asn Met Ser Ser Met Met Glu Glu Thr Pro Pro Leu 325 330 335	1008

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atg caa caa caa ggt ggt gtg tta gga gat gga tta ttc aga acg aca
 Met Gln Gln Gln Gly Gly Val Leu Gly Asp Gly Leu Phe Arg Thr Thr
 340 345 350

tgc tac caa tta ccc ggt tta aat tgg tac tct tct taa
 Ser Tyr Gln Leu Pro Gly Leu Asn Trp Tyr Ser Ser
 355 360

<210> SEQ ID NO 54
 <211> LENGTH: 364
 <212> TYPE: PRT
 <213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 54

Met Glu Ser Thr Asp Ser Ser Gly Gly Pro Pro Pro Gln Pro Asn
 1 5 10 15

Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Val Val
 20 25 30

His Tyr Leu Lys Arg Lys Ala Ala Ser Ala Pro Leu Pro Val Ala Ile
 35 40 45

Ile Ala Glu Val Asp Leu Tyr Lys Phe Asp Pro Trp Glu Leu Pro Ala
 50 55 60

Lys Ala Ser Phe Gly Glu Gln Glu Trp Tyr Phe Phe Ser Pro Arg Asp
 65 70 75 80

Arg Lys Tyr Pro Asn Gly Ala Arg Pro Asn Arg Ala Ala Thr Ser Gly
 85 90 95

Tyr Trp Lys Ala Thr Gly Thr Asp Lys Pro Val Leu Ala Ser Asp Gly
 100 105 110

Asn Gln Lys Val Gly Val Lys Lys Ala Leu Val Phe Tyr Ser Gly Lys
 115 120 125

Pro Pro Lys Gly Val Lys Ser Asp Trp Ile Met His Glu Tyr Arg Leu
 130 135 140

Ile Glu Asn Lys Pro Asn Asn Arg Pro Pro Gly Cys Asp Phe Gly Asn
 145 150 155 160

Lys Lys Asn Ser Leu Arg Leu Asp Asp Trp Val Leu Cys Arg Ile Tyr
 165 170 175

Lys Lys Asn Asn Ala Ser Arg His Val Asp Asn Asp Lys Asp His Asp
 180 185 190

Met Ile Asp Tyr Ile Phe Arg Lys Ile Pro Pro Ser Leu Ser Met Ala
 195 200 205

Ala Ala Ser Thr Gly Leu His Gln His His Asn Val Ser Arg Ser
 210 215 220

Met Asn Phe Phe Pro Gly Lys Phe Ser Gly Gly Tyr Gly Ile Phe
 225 230 235 240

Ser Asp Gly Gly Asn Thr Ser Ile Tyr Asp Gly Gly Met Ile Asn
 245 250 255

Asn Ile Gly Thr Asp Ser Val Asp His Asp Asn Asn Ala Asp Val Val
 260 265 270

Gly Leu Asn His Ala Ser Ser Ser Gly Pro Met Met Met Ala Asn Leu
 275 280 285

Lys Arg Thr Leu Pro Val Pro Tyr Trp Pro Val Ala Asp Glu Glu Gln
 290 295 300

Asp Ala Ser Pro Ser Lys Arg Phe His Gly Val Gly Gly Gly Gly
 305 310 315 320

Asp Cys Ser Asn Met Ser Ser Met Met Glu Glu Thr Pro Pro Leu
 325 330 335

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Met Gln Gln Gln Gly Gly Val Leu Gly Asp Gly Leu Phe Arg Thr Thr
 340 345 350

Ser Tyr Gln Leu Pro Gly Leu Asn Trp Tyr Ser Ser
 355 360

<210> SEQ ID NO 55
 <211> LENGTH: 1071
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1) .. (1071)

<400> SEQUENCE: 55

atg gcg aca att cag aag ctt gaa gaa gtt gca ggc aaa gat caa act	48
Met Ala Thr Ile Gln Lys Leu Glu Glu Val Ala Gly Lys Asp Gln Thr	
1 5 10 15	
cta aga gcc gtt gat cta acc atc atc aac ggc gtc aga aac gtc gaa	96
Leu Arg Ala Val Asp Leu Thr Ile Ile Asn Gly Val Arg Asn Val Glu	
20 25 30	
act tca aga cct ttc caa gta aat ccc aca gtg agt ctc gag ccc aag	144
Thr Ser Arg Pro Phe Gln Val Asn Pro Thr Val Ser Leu Glu Pro Lys	
35 40 45	
gcg gag ccg gtg atg ccg tgg ttt tca atg tct tta gct cca ccg tct	192
Ala Glu Pro Val Met Pro Ser Met Ser Leu Ala Pro Pro Ser	
50 55 60	
tcg aca gga cca cca ttg aag aga gct tcg act aaa gac cgt cac acg	240
Ser Thr Gly Pro Pro Leu Lys Arg Ala Ser Thr Lys Asp Arg His Thr	
65 70 75 80	
aag gtt gaa gga aga ggg aga agg ata ccg atg cct gcc acg tgt gcg	288
Lys Val Glu Gly Arg Arg Ile Arg Met Pro Ala Thr Cys Ala	
85 90 95	
gct agg att ttt caa tta act cga gag tta ggt cac aaa tcc gac ggc	336
Ala Arg Ile Phe Gln Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly	
100 105 110	
gaa acg att ccg tgg ttg gag aac gct gag ccg gcg att ata gcc	384
Glu Thr Ile Arg Trp Leu Leu Asn Ala Glu Pro Ala Ile Ile Ala	
115 120 125	
gcc acg ggt acg gga acg gtt ccc gcc atc gcc atg tcg gtt aac gga	432
Ala Thr Gly Thr Gly Thr Val Pro Ala Ile Ala Met Ser Val Asn Gly	
130 135 140	
acc tta aaa atc ccg acg acg aac gct gat tct gat atg ggt gaa	480
Thr Leu Lys Ile Pro Thr Thr Thr Asn Ala Asp Ser Asp Met Gly Glu	
145 150 155 160	
aat ctg atg aag aag aaa cgt aaa cga cct tct aac agt gag tat ata	528
Asn Leu Met Lys Lys Arg Lys Arg Pro Ser Asn Ser Glu Tyr Ile	
165 170 175	
gac ata agc gac gcc gtt tca gct tcc tcc ggt tta gct cca att gcc	576
Asp Ile Ser Asp Ala Val Ser Ala Ser Ser Gly Leu Ala Pro Ile Ala	
180 185 190	
acg acg aca acg atc caa cct ccg caa gct ctg gca tca tcc act gtg	624
Thr Thr Thr Ile Gln Pro Pro Gln Ala Leu Ala Ser Ser Thr Val	
195 200 205	
gct cag caa ctt ctg ccg caa gga atg tat ccg atg tgg gct att cca	672
Ala Gln Gln Leu Leu Pro Gln Gly Met Tyr Pro Met Trp Ala Ile Pro	
210 215 220	
tca aac gca atg att ccg acg gtc gga gct ttc ttg att cca caa	720
Ser Asn Ala Met Ile Pro Thr Val Gly Ala Phe Phe Leu Ile Pro Gln	
225 230 235 240	

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atc gct ggt ccg tcg aat cag cct cag tta tta gct ttt ccc gcc gcc Ile Ala Gly Pro Ser Asn Gln Pro Gln Leu Leu Ala Phe Pro Ala Ala 245 250 255	768
gct gct tcg ccg tcg tct tac gtc gcc gct gtt caa cag gct tcc acg Ala Ala Ser Pro Ser Ser Tyr Val Ala Ala Val Gln Gln Ala Ser Thr 260 265 270	816
atg gct aga cca cct cct tta caa gtt gtc cca agc agc ggc ttt gta Met Ala Arg Pro Pro Pro Leu Gln Val Val Pro Ser Ser Gly Phe Val 275 280 285	864
tcc gtt tca gac gtt agc ggt tcg aat tta tca aga gcg acg tcg gtt Ser Val Ser Asp Val Ser Gly Ser Asn Leu Ser Arg Ala Thr Ser Val 290 295 300	912
atg gct ccg agc tca agc tca ggc gta aca acc ggt agt tca tcg tca Met Ala Pro Ser Ser Ser Gly Val Thr Thr Gly Ser Ser Ser Ser 305 310 315 320	960
att gca aca aca acg acg cac acg ctg aga gac ttc tcc cta gag ata Ile Ala Thr Thr Thr His Thr Leu Arg Asp Phe Ser Leu Glu Ile 325 330 335	1008
tac gag aaa caa gag ctt cac cag ttc atg agc acc aca aca gca cg Tyr Glu Lys Gln Glu Leu His Gln Phe Met Ser Thr Thr Ala Arg 340 345 350	1056
tca tcg aac cac tga Ser Ser Asn His 355	1071

<210> SEQ ID NO 56
<211> LENGTH: 356
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 56

Met Ala Thr Ile Gln Lys Leu Glu Glu Val Ala Gly Lys Asp Gln Thr 1 5 10 15
Leu Arg Ala Val Asp Leu Thr Ile Ile Asn Gly Val Arg Asn Val Glu 20 25 30
Thr Ser Arg Pro Phe Gln Val Asn Pro Thr Val Ser Leu Glu Pro Lys 35 40 45
Ala Glu Pro Val Met Pro Ser Phe Ser Met Ser Leu Ala Pro Pro Ser 50 55 60
Ser Thr Gly Pro Pro Leu Lys Arg Ala Ser Thr Lys Asp Arg His Thr 65 70 75 80
Lys Val Glu Gly Arg Gly Arg Arg Ile Arg Met Pro Ala Thr Cys Ala 85 90 95
Ala Arg Ile Phe Gln Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly 100 105 110
Glu Thr Ile Arg Trp Leu Leu Glu Asn Ala Glu Pro Ala Ile Ile Ala 115 120 125
Ala Thr Gly Thr Gly Thr Val Pro Ala Ile Ala Met Ser Val Asn Gly 130 135 140
Thr Leu Lys Ile Pro Thr Thr Thr Asn Ala Asp Ser Asp Met Gly Glu 145 150 155 160
Asn Leu Met Lys Lys Arg Lys Arg Pro Ser Asn Ser Glu Tyr Ile 165 170 175
Asp Ile Ser Asp Ala Val Ser Ala Ser Ser Gly Leu Ala Pro Ile Ala 180 185 190
Thr Thr Thr Thr Ile Gln Pro Pro Gln Ala Leu Ala Ser Ser Thr Val 195 200 205

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Ala Gln Gln Leu Leu Pro Gln Gly Met Tyr Pro Met Trp Ala Ile Pro
 210 215 220
 Ser Asn Ala Met Ile Pro Thr Val Gly Ala Phe Phe Leu Ile Pro Gln
 225 230 235 240
 Ile Ala Gly Pro Ser Asn Gln Pro Gln Leu Leu Ala Phe Pro Ala Ala
 245 250 255
 Ala Ala Ser Pro Ser Ser Tyr Val Ala Ala Val Gln Gln Ala Ser Thr
 260 265 270
 Met Ala Arg Pro Pro Pro Leu Gln Val Val Pro Ser Ser Gly Phe Val
 275 280 285
 Ser Val Ser Asp Val Ser Gly Ser Asn Leu Ser Arg Ala Thr Ser Val
 290 295 300
 Met Ala Pro Ser Ser Ser Gly Val Thr Thr Gly Ser Ser Ser Ser
 305 310 315 320
 Ile Ala Thr Thr Thr His Thr Leu Arg Asp Phe Ser Leu Glu Ile
 325 330 335
 Tyr Glu Lys Gln Glu Leu His Gln Phe Met Ser Thr Thr Ala Arg
 340 345 350
 Ser Ser Asn His
 355

<210> SEQ_ID NO 57
 <211> LENGTH: 732
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(732)

<400> SEQUENCE: 57

atg gaa tat tcc caa tct tcc atg tat tca tct cca agt tct tgg agc	48
Met Glu Tyr Ser Gln Ser Ser Met Tyr Ser Ser Pro Ser Ser Trp Ser	
1 5 10 15	
tca tca caa gaa tca ctc tta tgg aac gag agc tgt ttc ttg gat caa	96
Ser Ser Gln Glu Ser Leu Trp Asn Glu Ser Cys Phe Leu Asp Gln	
20 25 30	
tca tct gaa cct caa gcc ttc ttt tgc cct aat tat gat tac tcc gat	144
Ser Ser Glu Pro Gln Ala Phe Phe Cys Pro Asn Tyr Asp Tyr Ser Asp	
35 40 45	
gac ttt ttc tca ttt gag tca ccg gag atg atg att aag gaa gaa att	192
Asp Phe Phe Ser Phe Glu Ser Pro Glu Met Met Ile Lys Glu Glu Ile	
50 55 60	
caa aac ggc gac gtt tct aac tcc gaa gaa gaa aag gtt gga att	240
Gln Asn Gly Asp Val Ser Asn Ser Glu Glu Glu Lys Val Gly Ile	
65 70 75 80	
gat gaa gaa aga tca tac aga gga gtg agg aaa agg ccg tgg ggg aaa	288
Asp Glu Glu Arg Ser Tyr Arg Gly Val Arg Lys Arg Pro Trp Gly Lys	
85 90 95	
ttt gca gcg gag ata aga gat tca acg agg aat gga att agg gtt tgg	336
Phe Ala Ala Glu Ile Arg Asp Ser Thr Arg Asn Gly Ile Arg Val Trp	
100 105 110	
ctc ggg aca ttt gac aaa gcc gag gaa gcc gct ctt gct tat gat caa	384
Leu Gly Thr Phe Asp Lys Ala Glu Glu Ala Ala Leu Ala Tyr Asp Gln	
115 120 125	
gcg gct ttc gcc aca aaa gga tct ctt gca aca ctt aat ttc ccg gtg	432
Ala Ala Phe Ala Thr Lys Gly Ser Leu Ala Thr Leu Asn Phe Pro Val	
130 135 140	

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gaa gtg gtt aga gag tcg cta aag aaa atg gag aat gtg aat ctt cat	480
Glu Val Val Arg Glu Ser Leu Lys Lys Met Glu Asn Val Asn Leu His	
145 150 155 160	
gat gga gga tct ccg gtt atg gcc ttg aag aga aaa cat tct ctt cga	528
Asp Gly Gly Ser Pro Val Met Ala Leu Lys Arg Lys His Ser Leu Arg	
165 170 175	
aac cgg cct aga ggg aaa aag cga tcc tct tct tct tct tct tct	576
Asn Arg Pro Arg Gly Lys Lys Arg Ser Ser Ser Ser Ser Ser Ser Ser	
180 185 190	
tct aat tct tct tgc tct tct tcg tct act tct tca aca tca	624
Ser Asn Ser Ser Cys Ser Ser Ser Ser Thr Ser Ser Thr Ser	
195 200 205	
aga agt agt agt aag cag agt gtt gtg aag caa gaa agt ggt aca ctt	672
Arg Ser Ser Lys Gln Ser Val Val Lys Gln Glu Ser Gly Thr Leu	
210 215 220	
gtg gtt ttt gaa gat tta ggt gct gag tat tta gaa caa ctt ctt atg	720
Val Val Phe Glu Asp Leu Gly Ala Glu Tyr Leu Glu Gln Leu Leu Met	
225 230 235 240	
agc tca tgt tga	732
Ser Ser Cys	

<210> SEQ ID NO: 58

<211> LENGTH: 243

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 58

Met Glu Tyr Ser Gln Ser Ser Met Tyr Ser Ser Pro Ser Ser Trp Ser	
1 5 10 15	
Ser Ser Gln Glu Ser Leu Leu Trp Asn Glu Ser Cys Phe Leu Asp Gln	
20 25 30	
Ser Ser Glu Pro Gln Ala Phe Phe Cys Pro Asn Tyr Asp Tyr Ser Asp	
35 40 45	
Asp Phe Phe Ser Phe Glu Ser Pro Glu Met Met Ile Lys Glu Glu Ile	
50 55 60	
Gln Asn Gly Asp Val Ser Asn Ser Glu Glu Glu Lys Val Gly Ile	
65 70 75 80	
Asp Glu Glu Arg Ser Tyr Arg Gly Val Arg Lys Arg Pro Trp Gly Lys	
85 90 95	
Phe Ala Ala Glu Ile Arg Asp Ser Thr Arg Asn Gly Ile Arg Val Trp	
100 105 110	
Leu Gly Thr Phe Asp Lys Ala Glu Ala Ala Leu Ala Tyr Asp Gln	
115 120 125	
Ala Ala Phe Ala Thr Lys Gly Ser Leu Ala Thr Leu Asn Phe Pro Val	
130 135 140	
Glu Val Val Arg Glu Ser Leu Lys Lys Met Glu Asn Val Asn Leu His	
145 150 155 160	
Asp Gly Gly Ser Pro Val Met Ala Leu Lys Arg Lys His Ser Leu Arg	
165 170 175	
Asn Arg Pro Arg Gly Lys Lys Arg Ser Ser Ser Ser Ser Ser Ser	
180 185 190	
Ser Asn Ser Ser Ser Cys Ser Ser Ser Ser Thr Ser Ser Thr Ser	
195 200 205	
Arg Ser Ser Ser Lys Gln Ser Val Val Lys Gln Glu Ser Gly Thr Leu	
210 215 220	
Val Val Phe Glu Asp Leu Gly Ala Glu Tyr Leu Glu Gln Leu Leu Met	
225 230 235 240	

Ser Ser Cys

<210> SEQ ID NO 59
<211> LENGTH: 1188
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1188)

<400> SEQUENCE: 59

atg aat tca ttt tcc cac gtc cct ccg ggt ttt aga ttt cac ccg aca	48
Met Asn Ser Phe Ser His Val Pro Pro Gly Phe Arg Phe His Pro Thr	
5 10 15	
gat gaa gaa ctt gta gac tac tac ctg agg aaa aaa gtc gca tcg aag	96
Asp Glu Glu Leu Val Asp Tyr Tyr Leu Arg Lys Lys Val Ala Ser Lys	
20 25 30	
aga ata gaa att gat ttc ata aag gac att gat ctt tac aag att gag	144
Arg Ile Glu Ile Asp Phe Ile Lys Asp Ile Asp Leu Tyr Lys Ile Glu	
35 40 45	
cca tgg gac ctt caa gag ttg tgc aaa att ggg cat gaa gag cag agt	192
Pro Trp Asp Leu Gln Glu Leu Cys Lys Ile Gly His Glu Glu Gln Ser	
50 55 60	
gat tgg tac ttc ttt agc cat aaa gac aag aag tat ccc aca ggg act	240
Asp Trp Tyr Phe Ser His Lys Asp Lys Tyr Pro Thr Gly Thr	
65 70 75 80	
cga acc aat aga gca aca aaa gca ggg ttt tgg aaa gcc acc gga aga	288
Arg Thr Asn Arg Ala Thr Lys Ala Gly Phe Trp Lys Ala Thr Gly Arg	
85 90 95	
gat aag gct atc tat ttg agg cat agt cta att ggc atg agg aaa aca	336
Asp Lys Ala Ile Tyr Leu Arg His Ser Leu Ile Gly Met Arg Lys Thr	
100 105 110	
ctt gtg ttt tac aag gga aga gcc cca aat gga caa aag tct gat tgg	384
Leu Val Phe Tyr Lys Gly Arg Ala Pro Asn Gly Gln Lys Ser Asp Trp	
115 120 125	
atc atg cac gaa tac cgc tta gaa acc gat gaa aac gga act cct cag	432
Ile Met His Glu Tyr Arg Leu Glu Thr Asp Glu Asn Gly Thr Pro Gln	
130 135 140	
gaa gaa gga tgg gtt gtg tgt agg gtt ttc aag aag aga ttg gct gca	480
Glu Glu Gly Trp Val Val Cys Arg Val Phe Lys Lys Arg Leu Ala Ala	
145 150 155 160	
gtt aga cga atg gga gat tac gac tca tcc cct tca cat tgg tac gat	528
Val Arg Arg Met Gly Asp Tyr Asp Ser Ser Pro Ser His Trp Tyr Asp	
165 170 175	
gat caa ctt tct ttt atg gcc tcc gag ctc gag aca aac ggt caa cga	576
Asp Gln Leu Ser Phe Met Ala Ser Glu Leu Glu Thr Asn Gly Gln Arg	
180 185 190	
cgg att ctc ccc aat cat cat cag cag cag cag cac cac caa caa	624
Arg Ile Leu Pro Asn His His Gln Gln Gln His Glu His Gln Gln	
195 200 205	
cat atg cca tat ggc ctc aat gca tct gct tac gct ctc aac aac cct	672
His Met Pro Tyr Gly Leu Asn Ala Ser Ala Tyr Ala Leu Asn Asn Pro	
210 215 220	
aac ttg caa tgc aag caa gag cta gaa cta cac tac aac cac ctg gta	720
Asn Leu Gln Cys Lys Gln Glu Leu Glu His Tyr Asn His Leu Val	
225 230 235 240	
caa cga aat cat ctt ctt gat gaa tct cat tta tcg ttc ctc caa ctt	768
Gln Arg Asn His Leu Leu Asp Glu Ser His Leu Ser Phe Leu Gln Leu	
245 250 255	

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cct caa cta gaa agc cct aag att caa caa gat aac agt aat tgc aac Pro Gln Leu Glu Ser Pro Lys Ile Gln Gln Asp Asn Ser Asn Cys Asn 260 265 270	816
tct ctt cct tat gga aca agc aac atc gat aat aac tcg agc cat aat Ser Leu Pro Tyr Gly Thr Ser Asn Ile Asp Asn Asn Ser Ser His Asn 275 280 285	864
gct aac ttg cag caa tca aat atc gcg cat gag gaa caa ttg aat caa Ala Asn Leu Gln Gln Ser Asn Ile Ala His Glu Gln Leu Asn Gln 290 295 300	912
gga aat cag aac ttc agc tct cta tac atg aac agc ggc aac gag caa Gly Asn Gln Asn Phe Ser Ser Leu Tyr Met Asn Ser Gly Asn Glu Gln 305 310 315 320	960
gtg atg gac caa gtc aca gac tgg aga gtt ctc gat aaa ttt gtt gct Val Met Asp Gln Val Thr Asp Trp Arg Val Leu Asp Lys Phe Val Ala 325 330 335	1008
tct cag cta agc aac gag gag gct gcc aca gct tct gca tct ata cag Ser Gln Leu Ser Asn Glu Glu Ala Ala Thr Ala Ser Ala Ser Ile Gln 340 345 350	1056
aat aat gcc aag gac aca agc aat gct gag tac caa gtt gat gaa gaa Asn Asn Ala Lys Asp Thr Ser Asn Ala Glu Tyr Gln Val Asp Glu Glu 355 360 365	1104
aaa gat ccg aaa agg gct tca gac atg gga gaa gaa tat act gct tct Lys Asp Pro Lys Arg Ala Ser Asp Met Gly Glu Glu Tyr Thr Ala Ser 370 375 380	1152
act tct tcg agt tgt cag att gat cta tgg aag tga Thr Ser Ser Cys Gln Ile Asp Leu Trp Lys 385 390 395	1188

<210> SEQ_ID NO 60
<211> LENGTH: 395
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 60

Met Asn Ser Phe Ser His Val Pro Pro Gly Phe Arg Phe His Pro Thr 1 5 10 15
Asp Glu Glu Leu Val Asp Tyr Tyr Leu Arg Lys Lys Val Ala Ser Lys 20 25 30
Arg Ile Glu Ile Asp Phe Ile Lys Asp Ile Asp Leu Tyr Lys Ile Glu 35 40 45
Pro Trp Asp Leu Gln Glu Leu Cys Lys Ile Gly His Glu Gln Ser 50 55 60
Asp Trp Tyr Phe Phe Ser His Lys Asp Lys Lys Tyr Pro Thr Gly Thr 65 70 75 80
Arg Thr Asn Arg Ala Thr Lys Ala Gly Phe Trp Lys Ala Thr Gly Arg 85 90 95
Asp Lys Ala Ile Tyr Leu Arg His Ser Leu Ile Gly Met Arg Lys Thr 100 105 110
Leu Val Phe Tyr Lys Gly Arg Ala Pro Asn Gly Gln Lys Ser Asp Trp 115 120 125
Ile Met His Glu Tyr Arg Leu Glu Thr Asp Glu Asn Gly Thr Pro Gln 130 135 140
Glu Glu Gly Trp Val Val Cys Arg Val Phe Lys Lys Arg Leu Ala Ala 145 150 155 160
Val Arg Arg Met Gly Asp Tyr Asp Ser Ser Pro Ser His Trp Tyr Asp 165 170 175
Asp Gln Leu Ser Phe Met Ala Ser Glu Leu Glu Thr Asn Gly Gln Arg 180 185 190

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Arg Ile Leu Pro Asn His His Gln Gln Gln Gln His Glu His Gln Gln
195 200 205

His Met Pro Tyr Gly Leu Asn Ala Ser Ala Tyr Ala Leu Asn Asn Pro
210 215 220

Asn Leu Gln Cys Lys Gln Glu Leu Glu Leu His Tyr Asn His Leu Val
225 230 235 240

Gln Arg Asn His Leu Leu Asp Glu Ser His Leu Ser Phe Leu Gln Leu
245 250 255

Pro Gln Leu Glu Ser Pro Lys Ile Gln Gln Asp Asn Ser Asn Cys Asn
260 265 270

Ser Leu Pro Tyr Gly Thr Ser Asn Ile Asp Asn Asn Ser Ser His Asn
275 280 285

Ala Asn Leu Gln Gln Ser Asn Ile Ala His Glu Glu Gln Leu Asn Gln
290 295 300

Gly Asn Gln Asn Phe Ser Ser Leu Tyr Met Asn Ser Gly Asn Glu Gln
305 310 315 320

Val Met Asp Gln Val Thr Asp Trp Arg Val Leu Asp Lys Phe Val Ala
325 330 335

Ser Gln Leu Ser Asn Glu Glu Ala Ala Thr Ala Ser Ala Ser Ile Gln
340 345 350

Asn Asn Ala Lys Asp Thr Ser Asn Ala Glu Tyr Gln Val Asp Glu Glu
355 360 365

Lys Asp Pro Lys Arg Ala Ser Asp Met Gly Glu Glu Tyr Thr Ala Ser
370 375 380

Thr Ser Ser Ser Cys Gln Ile Asp Leu Trp Lys
385 390 395

<210> SEQ ID NO 61
<211> LENGTH: 1005
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1005)

<400> SEQUENCE: 61

atg aac ata tca gta aac gga cag tca caa gta cct cct ggc ttt agg	48
Met Asn Ile Ser Val Asn Gly Gln Ser Gln Val Pro Pro Gly Phe Arg	
1 5 10 15	
ttt cac cca acc gag gaa gag ctc ttg aag tat tac ctc cgc aag aaa	96
Phe His Pro Thr Glu Glu Leu Leu Lys Tyr Tyr Leu Arg Lys Lys	
20 25 30	
atc tct aac atc aag atc gat ctc gat gtt att cct gac att gat ctc	144
Ile Ser Asn Ile Lys Ile Asp Leu Asp Val Ile Pro Asp Ile Asp Leu	
35 40 45	
aac aag ctc gag cct tgg gat att caa gag atg tgt aag att gga acg	192
Asn Lys Leu Glu Pro Trp Asp Ile Gln Glu Met Cys Lys Ile Gly Thr	
50 55 60	
acg ccg caa aac gat tgg tac ttt tat agc cat aag gac aag aag tat	240
Thr Pro Gln Asn Asp Trp Tyr Phe Tyr Ser His Lys Asp Lys Lys Tyr	
65 70 75 80	
ccc acc ggg act aga acc aac aga gcc acc acg gtc gga ttt tgg aaa	288
Pro Thr Gly Thr Arg Asn Arg Ala Thr Thr Val Gly Phe Trp Lys	
85 90 95	
gcg acg gga cgt gac aag acc ata tat acc aat ggt gat aga atc ggg	336
Ala Thr Gly Arg Asp Lys Thr Ile Tyr Thr Asn Gly Asp Arg Ile Gly	
100 105 110	

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atg cga aag acg ctt gtc ttc tac aaa ggt cga gcc cct cat ggt cag Met Arg Lys Thr Leu Val Phe Tyr Lys Gly Arg Ala Pro His Gly Gln 115 120 125	384
aaa tcc gat tgg atc atg cac gaa tat aga ctc gac gag agt gta tta Lys Ser Asp Trp Ile Met His Glu Tyr Arg Leu Asp Glu Ser Val Leu 130 135 140	432
atc tcc tcg tgt ggc gat cat gac gtc aac gta gaa acg tgt gat gtc Ile Ser Ser Cys Gly Asp His Asp Val Asn Val Glu Thr Cys Asp Val 145 150 155 160	480
ata gga agt gac gaa gga tgg gtg tgt cgt gtt ttc aag aaa aat Ile Gly Ser Asp Glu Gly Trp Val Val Cys Arg Val Phe Lys Lys Asn 165 170 175	528
aac ctt tgc aaa aac atg att agt agt agc ccg gcg agt tcg gtg aaa Asn Leu Cys Asn Met Ile Ser Ser Pro Ala Ser Ser Val Lys 180 185 190	576
acg ccg tcg ttc aat gag gag act atc gag caa ctt ctc gaa gtt atg Thr Pro Ser Phe Asn Glu Glu Thr Ile Glu Gln Leu Leu Glu Val Met 195 200 205	624
ggg caa tct tgt aaa gga gag ata gtt tta gac cct ttc tta aaa ctc Gly Gln Ser Cys Lys Gly Glu Ile Val Leu Asp Pro Phe Leu Lys Leu 210 215 220	672
cct aac ctc gaa tgc cat aac aac acc atc acg agt tat cag tgg Pro Asn Leu Glu Cys His Asn Asn Thr Thr Ile Thr Ser Tyr Gln Trp 225 230 235 240	720
tta atc gac gac caa gtc aac aac tgc cac gtc agc aaa gtt atg gat Leu Ile Asp Asp Gln Val Asn Asn Cys His Val Ser Lys Val Met Asp 245 250 255	768
ccc agc ttc atc act agc tgg gcc gct ttg gat cgg ctc gtt gcc tca Pro Ser Phe Ile Thr Ser Trp Ala Ala Leu Asp Arg Leu Val Ala Ser 260 265 270	816
cag tta aat ggg ccc aac tgc tat tca ata cca gcc gtt aat gag act Gln Leu Asn Gly Pro Asn Ser Tyr Ser Ile Pro Ala Val Asn Glu Thr 275 280 285	864
tca caa tca ccg tat cat gga ctg aac cgg tcc ggt tgt aat acc ggt Ser Gln Ser Pro Tyr His Gly Leu Asn Arg Ser Gly Cys Asn Thr Gly 290 295 300	912
tta aca cca gat tac tat ata ccg gag att gat tta tgg aac gag gca Leu Thr Pro Asp Tyr Tyr Ile Pro Glu Ile Asp Leu Trp Asn Glu Ala 305 310 315 320	960
gat ttc gcg aga acg aca tgc cac ttg ttg aac ggt agt gga taa Asp Phe Ala Arg Thr Thr Cys His Leu Leu Asn Gly Ser Gly 325 330	1005

<210> SEQ ID NO 62
<211> LENGTH: 334
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 62

Met Asn Ile Ser Val Asn Gly Gln Ser Gln Val Pro Pro Gly Phe Arg 1 5 10 15
Phe His Pro Thr Glu Glu Leu Leu Lys Tyr Tyr Leu Arg Lys Lys 20 25 30
Ile Ser Asn Ile Lys Ile Asp Leu Asp Val Ile Pro Asp Ile Asp Leu 35 40 45
Asn Lys Leu Glu Pro Trp Asp Ile Gln Glu Met Cys Lys Ile Gly Thr 50 55 60
Thr Pro Gln Asn Asp Trp Tyr Phe Tyr Ser His Lys Asp Lys Lys Tyr 65 70 75 80

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Pro Thr Gly Thr Arg Thr Asn Arg Ala Thr Thr Val Gly Phe Trp Lys
85 90 95

Ala Thr Gly Arg Asp Lys Thr Ile Tyr Thr Asn Gly Asp Arg Ile Gly
100 105 110

Met Arg Lys Thr Leu Val Phe Tyr Lys Gly Arg Ala Pro His Gly Gln
115 120 125

Lys Ser Asp Trp Ile Met His Glu Tyr Arg Leu Asp Glu Ser Val Leu
130 135 140

Ile Ser Ser Cys Gly Asp His Asp Val Asn Val Glu Thr Cys Asp Val
145 150 155 160

Ile Gly Ser Asp Glu Gly Trp Val Val Cys Arg Val Phe Lys Lys Asn
165 170 175

Asn Leu Cys Lys Asn Met Ile Ser Ser Ser Pro Ala Ser Ser Val Lys
180 185 190

Thr Pro Ser Phe Asn Glu Glu Thr Ile Glu Gln Leu Leu Glu Val Met
195 200 205

Gly Gln Ser Cys Lys Gly Glu Ile Val Leu Asp Pro Phe Leu Lys Leu
210 215 220

Pro Asn Leu Glu Cys His Asn Asn Thr Thr Ile Thr Ser Tyr Gln Trp
225 230 235 240

Leu Ile Asp Asp Gln Val Asn Asn Cys His Val Ser Lys Val Met Asp
245 250 255

Pro Ser Phe Ile Thr Ser Trp Ala Ala Leu Asp Arg Leu Val Ala Ser
260 265 270

Gln Leu Asn Gly Pro Asn Ser Tyr Ser Ile Pro Ala Val Asn Glu Thr
275 280 285

Ser Gln Ser Pro Tyr His Gly Leu Asn Arg Ser Gly Cys Asn Thr Gly
290 295 300

Leu Thr Pro Asp Tyr Tyr Ile Pro Glu Ile Asp Leu Trp Asn Glu Ala
305 310 315 320

Asp Phe Ala Arg Thr Thr Cys His Leu Leu Asn Gly Ser Gly
325 330

<210> SEQ ID NO 63

<211> LENGTH: 792

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(792)

<400> SEQUENCE: 63

atg gcg aat tca gga aat tat gga aag agg ccc ttt cga ggc gat gaa	48
Met Ala Asn Ser Gly Asn Tyr Gly Lys Arg Pro Phe Arg Gly Asp Glu	
1 5 10 15	

tcg gat gaa aag aaa gaa gcc gat gat gat gag aac ata ttc cct ttc	96
Ser Asp Glu Lys Lys Glu Ala Asp Asp Asp Glu Asn Ile Phe Pro Phe	
20 25 30	

tcc tct gcc cga tcc caa tat gac atg cgt gcc atg gtc tca gcc ttg	144
Phe Ser Ala Arg Ser Gln Tyr Asp Met Arg Ala Met Val Ser Ala Leu	
35 40 45	

act caa gtc att gga aac caa agc agc tct cat gat aat aac caa cat	192
Thr Gln Val Ile Gly Asn Gln Ser Ser His Asp Asn Asn Gln His	
50 55 60	

caa cct gtt gtg tat aat caa caa gat cct aac cca ccg gct cct cca	240
Gln Pro Val Val Tyr Asn Gln Gln Asp Pro Asn Pro Pro Ala Pro Pro	
65 70 75 80	

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act caa gat caa ggg cta ttg agg aag agg cac tat aga ggg gta aga Thr Gln Asp Gln Gly Leu Leu Arg Lys Arg His Tyr Arg Gly Val Arg 85 90 95	288
caa cga cca tgg gga aag tgg gca gct gaa att cggttccg gat ccg caa aag Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Gln Lys 100 105 110	336
gca gca cgg gtg tgg ctc ggg aca ttt gag act gct gaa gct gcg gct Ala Ala Arg Val Trp Leu Gly Thr Phe Glu Thr Ala Glu Ala Ala Ala 115 120 125	384
tta gct tat gat aac gca gct ctt aag ttc aaa gga agc aaa gcc aaa Leu Ala Tyr Asp Asn Ala Ala Leu Lys Phe Lys Gly Ser Lys Ala Lys 130 135 140	432
ctc aat ttc cct gag aga gct caa cta gca agt aac act agt aca act Leu Asn Phe Pro Glu Arg Ala Gln Leu Ala Ser Asn Thr Ser Thr Thr 145 150 155 160	480
acc ggt cca cca aac tat tat tct tct aat aat caa att tac tac tca Thr Gly Pro Pro Tyr Tyr Ser Ser Asn Asn Gln Ile Tyr Tyr Ser 165 170 175	528
aat ccg cag act aat ccg caa acc ata cct tat ttt aac caa tac tac Asn Pro Gln Thr Asn Pro Gln Thr Ile Pro Tyr Phe Asn Gln Tyr Tyr 180 185 190	576
tat aac caa tat ctt cat caa ggg ggg aat agt aac gat gca tta agt Tyr Asn Gln Tyr Leu His Gln Gly Gly Asn Ser Asn Asp Ala Leu Ser 195 200 205	624
tat agc ttg gcc ggt gga gaa acc gga ggc tca atg tat aat cat cag Tyr Ser Leu Ala Gly Gly Glu Thr Gly Ser Met Tyr Asn His Gln 210 215 220	672
acg tta tct act aca aat tct tca tct tct ggt gga tct tca agg caa Thr Leu Ser Thr Thr Asn Ser Ser Ser Gly Gly Ser Ser Arg Gln 225 230 235 240	720
caa gat gat gaa caa gat tac gcc aga tat ttg cgt ttt ggg gat tct Gln Asp Asp Glu Gln Asp Tyr Ala Arg Tyr Leu Arg Phe Gly Asp Ser 245 250 255	768
tca cct cct aat tct ggt ttt tga Ser Pro Pro Asn Ser Gly Phe 260	792
<210> SEQ ID NO 64 <211> LENGTH: 263 <212> TYPE: PRT <213> ORGANISM: Arabidopsis thaliana	
<400> SEQUENCE: 64	
Met Ala Asn Ser Gly Asn Tyr Gly Lys Arg Pro Phe Arg Gly Asp Glu 1 5 10 15	
Ser Asp Glu Lys Lys Glu Ala Asp Asp Asp Glu Asn Ile Phe Pro Phe 20 25 30	
Phe Ser Ala Arg Ser Gln Tyr Asp Met Arg Ala Met Val Ser Ala Leu 35 40 45	
Thr Gln Val Ile Gly Asn Gln Ser Ser Ser His Asp Asn Asn Gln His 50 55 60	
Gln Pro Val Val Tyr Asn Gln Gln Asp Pro Asn Pro Pro Ala Pro Pro 65 70 75 80	
Thr Gln Asp Gln Gly Leu Leu Arg Lys Arg His Tyr Arg Gly Val Arg 85 90 95	
Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Gln Lys 100 105 110	
Ala Ala Arg Val Trp Leu Gly Thr Phe Glu Thr Ala Glu Ala Ala Ala 115 120 125	

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Leu Ala Tyr Asp Asn Ala Ala Leu Lys Phe Lys Gly Ser Lys Ala Lys
 130 135 140

Leu Asn Phe Pro Glu Arg Ala Gln Leu Ala Ser Asn Thr Ser Thr Thr
 145 150 155 160

Thr Gly Pro Pro Asn Tyr Tyr Ser Ser Asn Asn Gln Ile Tyr Tyr Ser
 165 170 175

Asn Pro Gln Thr Asn Pro Gln Thr Ile Pro Tyr Phe Asn Gln Tyr Tyr
 180 185 190

Tyr Asn Gln Tyr Leu His Gln Gly Asn Ser Asn Asp Ala Leu Ser
 195 200 205

Tyr Ser Leu Ala Gly Glu Thr Gly Ser Met Tyr Asn His Gln
 210 215 220

Thr Leu Ser Thr Thr Asn Ser Ser Ser Gly Gly Ser Ser Arg Gln
 225 230 235 240

Gln Asp Asp Glu Gln Asp Tyr Ala Arg Tyr Leu Arg Phe Gly Asp Ser
 245 250 255

Ser Pro Pro Asn Ser Gly Phe
 260

<210> SEQ_ID NO 65

<211> LENGTH: 1140

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1) .. (1140)

<400> SEQUENCE: 65

atg tgc gga gca atc atc tcc gat ttc atc cct ccg ccg agg tcc	48
Met Cys Gly Gly Ala Ile Ile Ser Asp Phe Ile Pro Pro Pro Arg Ser	
1 5 10 15	

ctc cgc gtc act aac gag ttt atc tgg ccg gat ctg aaa aac aaa gtg	96
Ley Arg Val Thr Asn Glu Phe Ile Trp Pro Asp Ley Lys Asn Lys Val	
20 25 30	

aaa gct tca aag aag aga tcg aat aag cga tcc gat ttc ttc gat ctt	144
Lys Ala Ser Lys Lys Arg Ser Asn Lys Arg Ser Asp Phe Phe Asp Ley	
35 40 45	

gac gat gat ttc gaa gct gat ttc caa ggg ttt aag gat gac tcg gct	192
Asp Asp Asp Phe Ala Asp Phe Gln Gly Phe Lys Asp Asp Ser Ala	
50 55 60	

ttt gac tgc gaa gac gat gat gat gtc ttc gtc aat gtt aag cct ttc	240
Phe Asp Cys Glu Asp Asp Asp Val Phe Val Asn Val Lys Pro Phe	
65 70 75 80	

gtc ttc acc gca act act aag ccc gta gct tcc gct ttc gtc tcc act	288
Val Phe Thr Ala Thr Lys Pro Val Ala Ser Ala Phe Val Ser Thr	
85 90 95	

ggt ata tat ttg gta ggt tca gca tat gcc aag aaa act gta gag tcc	336
Gly Ile Tyr Ley Val Gly Ser Ala Tyr Ala Lys Lys Thr Val Glu Ser	
100 105 110	

gct gag caa gct gag aaa tct tct aag agg aag agg aag aat cca tac	384
Ala Glu Gln Ala Glu Lys Ser Ser Lys Arg Lys Arg Lys Asn Gln Tyr	
115 120 125	

cga ggg att agg cag cgt cct tgg gga aaa tgg gct gcg gag atc cgt	432
Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg	
130 135 140	

gat ccg aga aaa ggc tcc cga gaa tgg ctt gga aca ttc gac act gct	480
Asp Pro Arg Lys Gly Ser Arg Glu Trp Ley Gly Thr Phe Asp Thr Ala	
145 150 155 160	

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gag gaa gca gca aga gct tat gat gct gca gca cgc aga atc cgt ggc Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg Ile Arg Gly 165 170 175	528
acg aaa gct aag gtg aat ttt ccc gag gag aag aac cct agc gtc gta Thr Lys Ala Lys Val Asn Phe Pro Glu Glu Lys Asn Pro Ser Val Val 180 185 190	576
tcc cag aaa cgt cct agt gct aag act aat aat ctt cag aaa tca gtg Ser Gln Lys Arg Pro Ser Ala Lys Thr Asn Asn Leu Gln Lys Ser Val 195 200 205	624
gct aaa cca aac aaa agc gta act ttg gtt cag cag cca aca cat ctg Ala Lys Pro Asn Lys Ser Val Thr Leu Val Gln Gln Pro Thr His Leu 210 215 220	672
agt cag cag tac tgc aac aac tcc ttt gac aac tct ttt ggt gat atg Ser Gln Gln Tyr Cys Asn Asn Ser Phe Asp Asn Ser Phe Gly Asp Met 225 230 235 240	720
agt ttc atg gaa gag aag cct cag atg tac aac aat cag ttt ggg tta Ser Phe Met Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu 245 250 255	768
aca aac tcg ttc gat gct gga ggt aac aat gga tac cag tat ttc agt Thr Asn Ser Phe Asp Ala Gly Gly Asn Asn Gly Tyr Gln Tyr Phe Ser 260 265 270	816
tcc gat cag ggc agt aac tcc ttc gac tgt tct gag ttc ggg tgg agt Ser Asp Gln Gly Ser Asn Ser Phe Asp Cys Ser Glu Phe Gly Trp Ser 275 280 285	864
gat cac ggc cct aaa aca ccc gag atc tct tca atg ctt gtc aat aac Asp His Gly Pro Lys Thr Pro Glu Ile Ser Ser Met Leu Val Asn Asn 290 295 300	912
aac gaa gca tca ttt gtt gaa gaa acc aat gca gcc aag aag ctc aaa Asn Glu Ala Ser Phe Val Glu Glu Thr Asn Ala Ala Lys Lys Leu Lys 305 310 315 320	960
cca aac tct gat gag tca gac gat ctg atg gca tac ctt gac aac gcc Pro Asn Ser Asp Glu Ser Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala 325 330 335	1008
ttg tgg gac acc cca cta gaa gtg gaa gcc atg ctt ggc gca gat gct Leu Trp Asp Thr Pro Leu Glu Val Glu Ala Met Leu Gly Ala Asp Ala 340 345 350	1056
ggt gct gtg act cag gaa gag gaa aac cca gtg gag cta tgg agc tta Gly Ala Val Thr Gln Glu Glu Asn Pro Val Glu Leu Trp Ser Leu 355 360 365	1104
gat gag atc aat ttc atg ctg gaa gga gac ttt tga Asp Glu Ile Asn Phe Met Leu Glu Gly Asp Phe 370 375	1140

<210> SEQ ID NO 66

<211> LENGTH: 379

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 66

Met Cys Gly Gly Ala Ile Ile Ser Asp Phe Ile Pro Pro Pro Arg Ser 1 5 10 15
Leu Arg Val Thr Asn Glu Phe Ile Trp Pro Asp Leu Lys Asn Lys Val 20 25 30
Lys Ala Ser Lys Lys Arg Ser Asn Lys Arg Ser Asp Phe Phe Asp Leu 35 40 45
Asp Asp Asp Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp Ser Ala 50 55 60
Phe Asp Cys Glu Asp Asp Asp Val Phe Val Asn Val Lys Pro Phe 65 70 75 80

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Val Phe Thr Ala Thr Thr Lys Pro Val Ala Ser Ala Phe Val Ser Thr
85 90 95

Gly Ile Tyr Leu Val Gly Ser Ala Tyr Ala Lys Lys Thr Val Glu Ser
100 105 110

Ala Glu Gln Ala Glu Lys Ser Ser Lys Arg Lys Arg Lys Asn Gln Tyr
115 120 125

Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg
130 135 140

Asp Pro Arg Lys Gly Ser Arg Glu Trp Leu Gly Thr Phe Asp Thr Ala
145 150 155 160

Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg Ile Arg Gly
165 170 175

Thr Lys Ala Lys Val Asn Phe Pro Glu Glu Lys Asn Pro Ser Val Val
180 185 190

Ser Gln Lys Arg Pro Ser Ala Lys Thr Asn Asn Leu Gln Lys Ser Val
195 200 205

Ala Lys Pro Asn Lys Ser Val Thr Leu Val Gln Gln Pro Thr His Leu
210 215 220

Ser Gln Gln Tyr Cys Asn Asn Ser Phe Asp Asn Ser Phe Gly Asp Met
225 230 235 240

Ser Phe Met Glu Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu
245 250 255

Thr Asn Ser Phe Asp Ala Gly Gly Asn Asn Gly Tyr Gln Tyr Phe Ser
260 265 270

Ser Asp Gln Gly Ser Asn Ser Phe Asp Cys Ser Glu Phe Gly Trp Ser
275 280 285

Asp His Gly Pro Lys Thr Pro Glu Ile Ser Ser Met Leu Val Asn Asn
290 295 300

Asn Glu Ala Ser Phe Val Glu Glu Thr Asn Ala Ala Lys Lys Leu Lys
305 310 315 320

Pro Asn Ser Asp Glu Ser Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala
325 330 335

Leu Trp Asp Thr Pro Leu Glu Val Glu Ala Met Leu Gly Ala Asp Ala
340 345 350

Gly Ala Val Thr Gln Glu Glu Asn Pro Val Glu Leu Trp Ser Leu
355 360 365

Asp Glu Ile Asn Phe Met Leu Glu Gly Asp Phe
370 375

<210> SEQ ID NO 67
<211> LENGTH: 738
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(738)

<400> SEQUENCE: 67

atg gag ttc aat ggt aat ttg aat gcc ggt tct tgc tct aga tca aaa	48
Met Glu Phe Asn Gly Asn Leu Asn Ala Gly Ser Cys Ser Arg Ser Lys	
1 5 10 15	
aag agt cat agg caa aag cag caa ccc cag cca cag cca caa caa	96
Lys Ser His Arg Gln Lys Gln Gln Pro Gln Pro Gln Gln	
20 25 30	
cat att gaa gaa ata aag tat gta gga gtg agg agg cca tgg gga	
His Ile Glu Glu Ile Lys Tyr Val Gly Val Arg Arg Pro Trp Gly	
35 40 45	

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aga tat gca gct gag ata aga aac ccg acg acg aaa gag agg tat tgg Arg Tyr Ala Ala Glu Ile Arg Asn Pro Thr Thr Lys Glu Arg Tyr Trp 50 55 60	192
cta ggt act ttt gac acg gcc gag gag gct gca ttg gct tat gat aga Leu Gly Thr Phe Asp Thr Ala Glu Ala Ala Leu Ala Tyr Asp Arg 65 70 75 80	240
gcc gca cgg tcc ata aga ggc ttg act gct cga acc aac ttt gtc tac Ala Ala Arg Ser Ile Arg Gly Leu Thr Ala Arg Thr Asn Phe Val Tyr 85 90 95	288
tcc gat atg cct cgt ggc tcc tca gta act tcc ttt gtg tct cct gat Ser Asp Met Pro Arg Gly Ser Ser Val Thr Ser Phe Val Ser Pro Asp 100 105 110	336
gaa tcc caa cgt ttc att tcc gag tta ttc aac cct cca agc caa cta Glu Ser Gln Arg Phe Ile Ser Glu Leu Phe Asn Pro Pro Ser Gln Leu 115 120 125	384
gaa gct act aac agc aac aat aac aac aat aac aat ctc tac tca tcg Glu Ala Thr Asn Ser Asn Asn Asn Asn Asn Asn Leu Tyr Ser Ser 130 135 140	432
acc aac aac caa aac cag aac tct att gag ttc tca tac aat ggg tgg Thr Asn Asn Gln Asn Asn Ser Ile Glu Phe Ser Tyr Asn Gly Trp 145 150 155 160	480
cct cag gag gct gaa tgt ggt tat caa tct ata acc agt aat gct gag Pro Gln Glu Ala Glu Cys Gly Tyr Gln Ser Ile Thr Ser Asn Ala Glu 165 170 175	528
cat tgt gat cat gag ctt cca cct ctt ccc agt act tgt ttt gga His Cys Asp His Glu Leu Pro Pro Ser Thr Cys Phe Gly 180 185 190	576
gct gaa ctg agg att ccg gag acg gat agc tat tgg aat gtt gcg cat Ala Glu Leu Arg Ile Pro Glu Thr Asp Ser Tyr Trp Asn Val Ala His 195 200 205	624
gca agc ata gac acg ttt gcc ttc gag ctt gat ggc ttt gtg gat caa Ala Ser Ile Asp Thr Phe Ala Phe Glu Leu Asp Gly Phe Val Asp Gln 210 215 220	672
aac agt ctt ggt cag agt gga aca gaa ggg ttt aat tct tta ccc tcc Asn Ser Leu Gly Gln Ser Gly Thr Glu Gly Phe Asn Ser Leu Pro Ser 225 230 235 240	720
aca ttc ttc tac caa taa Thr Phe Phe Tyr Gln 245	738

<210> SEQ ID NO 68
<211> LENGTH: 245
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 68

Met Glu Phe Asn Gly Asn Leu Asn Ala Gly Ser Cys Ser Arg Ser Lys 1 5 10 15
Lys Ser His Arg Gln Lys Gln Gln Pro Gln Pro Gln Pro Gln Gln 20 25 30
His Ile Glu Glu Ile Lys Tyr Val Gly Val Arg Arg Pro Trp Gly 35 40 45
Arg Tyr Ala Ala Glu Ile Arg Asn Pro Thr Thr Lys Glu Arg Tyr Trp 50 55 60
Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Arg 65 70 75 80
Ala Ala Arg Ser Ile Arg Gly Leu Thr Ala Arg Thr Asn Phe Val Tyr 85 90 95

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Ser Asp Met Pro Arg Gly Ser Ser Val Thr Ser Phe Val Ser Pro Asp
100 105 110

Glu Ser Gln Arg Phe Ile Ser Glu Leu Phe Asn Pro Pro Ser Gln Leu
115 120 125

Glu Ala Thr Asn Ser Asn Asn Asn Asn Asn Asn Leu Tyr Ser Ser
130 135 140

Thr Asn Asn Gln Asn Asn Ser Ile Glu Phe Ser Tyr Asn Gly Trp
145 150 155 160

Pro Gln Glu Ala Glu Cys Gly Tyr Gln Ser Ile Thr Ser Asn Ala Glu
165 170 175

His Cys Asp His Glu Leu Pro Pro Leu Pro Pro Ser Thr Cys Phe Gly
180 185 190

Ala Glu Leu Arg Ile Pro Glu Thr Asp Ser Tyr Trp Asn Val Ala His
195 200 205

Ala Ser Ile Asp Thr Phe Ala Phe Glu Leu Asp Gly Phe Val Asp Gln
210 215 220

Asn Ser Leu Gly Gln Ser Gly Thr Glu Gly Phe Asn Ser Leu Pro Ser
225 230 235 240

Thr Phe Phe Tyr Gln
245

<210> SEQ ID NO 69
<211> LENGTH: 771
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(771)

<400> SEQUENCE: 69

atg gga agg ggt agg gtt caa ttg aag agg ata gag aac aag atc aat Met Gly Arg Gly Arg Val Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn	48
1 5 10 15	
aga caa gtg aca ttc tcg aaa aga aga gct ggt ctt ttg aag aaa gct Arg Gln Val Thr Phe Ser Lys Arg Arg Ala Gly Leu Leu Lys Ala	96
20 25 30	
cat gag atc tct gtt ctc tgt gat gct gaa gtt gct ctt gtt gtc ttc His Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Val Phe	144
35 40 45	
tcc cat aag gga aaa ctc ttc gaa tac tcc act gat tct tgt atg gag Ser His Lys Gly Lys Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu	192
50 55 60	
aag ata ctt gaa cgc tat gag agg tac tct tac gcc gaa aga cag ctt Lys Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Arg Gln Leu	240
65 70 75 80	
att gca cct gag tcc gac gtc aat aca aac tgg tcg atg gag tat aac Ile Ala Pro Glu Ser Asp Val Asn Thr Asn Trp Ser Met Glu Tyr Asn	288
85 90 95	
agg ctt aag gct aag att gag ctt ttg gag aga aac cag agg cat tat Arg Leu Lys Ala Lys Ile Glu Leu Leu Glu Arg Asn Gln Arg His Tyr	336
100 105 110	
ctt ggg gaa gac ttg caa gca atg agc cct aaa gag ctt cag aat ctg Leu Gly Glu Asp Leu Gln Ala Met Ser Pro Lys Glu Leu Gln Asn Leu	384
115 120 125	
gag cag cag ctt gac act gct ctt aag cac atc cgc act aga aaa aac Glu Gln Gln Leu Asp Thr Ala Leu Lys His Ile Arg Thr Arg Lys Asn	432
130 135 140	

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180

caa ctt atg tac gag tcc atc aat gag ctc caa aaa aag gag aag gcc	480
Gln Leu Met Tyr Glu Ser Ile Asn Glu Leu Gln Lys Lys Glu Lys Ala	
145 150 155 160	
ata cag gag caa aac agc atg ctt tct aaa cag atc aag gag agg gaa	528
Ile Gln Gln Asn Ser Met Leu Ser Lys Gln Ile Lys Glu Arg Glu	
165 170 175	
aaa att ctt agg gct caa cag gag cag tgg gat cag cag aac caa ggc	576
Lys Ile Leu Arg Ala Gln Glu Gln Trp Asp Gln Gln Asn Gln Gly	
180 185 190	
cac aat atg cct ccc cct ctg cca ccg cag cag cac caa atc cag cat	624
His Asn Met Pro Pro Pro Leu Pro Pro Gln Gln His Gln Ile Gln His	
195 200 205	
cct tac atg ctc tct cat cag cca tct cct ttc ctc aac atg ggt ggt	672
Pro Tyr Met Leu Ser His Gln Pro Ser Pro Phe Leu Asn Met Gly Gly	
210 215 220	
ctg tat caa gaa gat gat cct atg gca atg agg agg aat gat ctc gaa	720
Leu Tyr Gln Glu Asp Asp Pro Met Ala Met Arg Arg Asn Asp Leu Glu	
225 230 235 240	
ctg act ctt gaa ccc gtt tac aac tgc aac ctt ggc tgc ttc gcc gca	768
Leu Thr Leu Glu Pro Val Tyr Asn Cys Asn Leu Gly Cys Phe Ala Ala	
245 250 255	
tga	771

<210> SEQ ID NO 70

<211> LENGTH: 256

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 70

Met Gly Arg Gly Arg Val Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn	
1 5 10 15	
Arg Gln Val Thr Phe Ser Lys Arg Arg Ala Gly Leu Leu Lys Ala	
20 25 30	
His Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Val Phe	
35 40 45	
Ser His Lys Gly Lys Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu	
50 55 60	
Lys Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Arg Gln Leu	
65 70 75 80	
Ile Ala Pro Glu Ser Asp Val Asn Thr Asn Trp Ser Met Glu Tyr Asn	
85 90 95	
Arg Leu Lys Ala Lys Ile Glu Leu Glu Arg Asn Gln Arg His Tyr	
100 105 110	
Leu Gly Glu Asp Leu Gln Ala Met Ser Pro Lys Glu Leu Gln Asn Leu	
115 120 125	
Glu Gln Gln Leu Asp Thr Ala Leu Lys His Ile Arg Thr Arg Lys Asn	
130 135 140	
Gln Leu Met Tyr Glu Ser Ile Asn Glu Leu Gln Lys Lys Glu Lys Ala	
145 150 155 160	
Ile Gln Glu Gln Asn Ser Met Leu Ser Lys Gln Ile Lys Glu Arg Glu	
165 170 175	
Lys Ile Leu Arg Ala Gln Gln Glu Gln Trp Asp Gln Gln Asn Gln Gly	
180 185 190	
His Asn Met Pro Pro Pro Leu Pro Pro Gln Gln His Gln Ile Gln His	
195 200 205	

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Pro	Tyr	Met	Leu	Ser	His	Gln	Pro	Ser	Pro	Phe	Leu	Asn	Met	Gly	Gly
210						215					220				

Leu	Tyr	Gln	Glu	Asp	Asp	Pro	Met	Ala	Met	Arg	Arg	Asn	Asp	Leu	Glu
225							230			235				240	

Leu	Thr	Leu	Glu	Pro	Val	Tyr	Asn	Cys	Asn	Leu	Gly	Cys	Phe	Ala	Ala
							245			250			255		

<210> SEQ_ID NO 71
<211> LENGTH: 1356
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1356)

<400> SEQUENCE: 71

atg	ggc	gaa	tct	gtg	gct	gtt	act	gcc	ccg	ccc	tcg	gct	act		48	
Met	Gly	Arg	Glu	Ser	Val	Ala	Val	Val	Ala	Pro	Pro	Ser	Ala	Thr		
1						5		10				15				
gct	ccg	ggt	act	gct	tcg	gtg	gct	acc	tcg	ctt	gct	cct	ggc	ttc	96	
Ala	Pro	Gly	Thr	Ala	Ser	Val	Ala	Thr	Ser	Leu	Ala	Pro	Gly	Phe	Arg	
						20		25			30					
ttt	cat	ccg	act	gat	gag	gaa	ctc	gtg	agc	tat	tac	ttg	aag	agg	aag	144
Phe	His	Pro	Thr	Asp	Glu	Glu	Leu	Val	Ser	Tyr	Tyr	Ley	Lys	Arg	Lys	
						35		40			45					
gtt	ctg	ggc	caa	cct	gta	cgc	ttc	gat	gct	att	gga	gag	gtc	gat	ata	192
Val	Leu	Gly	Gln	Pro	Val	Arg	Phe	Asp	Ala	Ile	Gly	Glu	Val	Asp	Ile	
						50		55			60					
tac	aag	cat	gag	ccc	tgg	gat	tta	gca	gtg	ttt	tcg	aga	ttg	aag	aac	240
Tyr	Lys	His	Glu	Pro	Trp	Asp	Leu	Ala	Val	Phe	Ser	Arg	Leu	Lys	Thr	
						65		70			75			80		
agg	gac	caa	gaa	tgg	tac	tgt	act	gca	tta	gat	aag	aag	tat	gga	288	
Arg	Asp	Gln	Glu	Trp	Tyr	Phe	Tyr	Ser	Ala	Ley	Asp	Lys	Lys	Tyr	Gly	
						85		90			95					
aac	ggt	gct	agg	atg	aac	cga	gca	act	aac	aga	ggg	tac	tgg	aaa	gct	336
Asn	Gly	Ala	Arg	Met	Asn	Arg	Ala	Thr	Asn	Arg	Gly	Tyr	Trp	Lys	Ala	
						100		105			110					
act	gga	aaa	gac	aga	gaa	atc	cgc	cgt	gac	att	ctg	ctt	ctc	ggc	atg	384
Thr	Gly	Lys	Asp	Arg	Glu	Ile	Arg	Arg	Asp	Ile	Ley	Ley	Ley	Gly	Met	
						115		120			125					
aaa	aag	aca	ctt	gtt	tcc	cac	agt	ggg	cgt	gca	cca	gac	ggg	ctt	cg	432
Lys	Lys	Thr	Leu	Val	Phe	His	Ser	Gly	Arg	Ala	Pro	Asp	Gly	Leu	Arg	
						130		135			140					
act	aat	tgg	gtt	atg	cat	gag	tat	cgc	ctt	gtg	gaa	tat	gaa	acc	gag	480
Thr	Asn	Trp	Val	Met	His	Glu	Tyr	Arg	Leu	Val	Glu	Tyr	Glu	Thr	Glu	
						145		150			155			160		
aaa	aac	gga	aac	ctg	gtg	caa	gat	gca	tat	gtg	ttg	tgt	aga	gtc	ttc	528
Lys	Asn	Gly	Asn	Leu	Val	Gln	Asp	Ala	Tyr	Val	Ley	Cys	Arg	Val	Phe	
						165		170			175					
cac	aag	aat	aac	att	ggg	cca	cca	agt	ggg	aac	aga	tat	gct	ccg	ttc	576
His	Lys	Asn	Asn	Ile	Gly	Pro	Pro	Ser	Gly	Asn	Arg	Tyr	Ala	Pro	Phe	
						180		185			190					
atg	gaa	gag	gaa	tgg	gtt	gat	gat	gaa	gga	gct	ctg	att	cca	gga	ata	624
Met	Glu	Glu	Trp	Ala	Asp	Asp	Glu	Gly	Ala	Leu	Ile	Pro	Gly	Ile		
						195		200			205					
gac	gtt	aag	ctc	agg	cta	gag	ccg	ccg	cca	gta	gcc	aat	gga	aac	gac	672
Asp	Val	Lys	Leu	Arg	Leu	Glu	Pro	Pro	Pro	Val	Ala	Asn	Gly	Asn	Asp	
						210		215			220					
cag	atg	gac	cag	aat	atc	cag	tca	gcc	agc	aag	agt	ctc	atc	aac	atc	720
Gln	Met	Asp	Gln	Ile	Glu	Gln	Ser	Ala	Ser	Lys	Ser	Leu	Ile	Asn	Ile	
						225		230			235			240		

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aat gag cca ccg aga gag aca gct cca ctg gat atc gaa tcg gac caa Asn Glu Pro Pro Arg Glu Thr Ala Pro Leu Asp Ile Glu Ser Asp Gln 245 250 255	768
cag aat cat cat gag aat gac ctc aag ccg gag gag cat aac aac aat Gln Asn His His Glu Asn Asp Leu Lys Pro Glu Glu His Asn Asn Asn 260 265 270	816
aat aat tat gat gaa aac gag gaa aca ctc aaa cgc gag cag atg gaa Asn Asn Tyr Asp Glu Asn Glu Glu Thr Leu Lys Arg Glu Gln Met Glu 275 280 285	864
gaa gag gag cgt cct cct cga cct gta tgc gtt ctc aac aaa gaa gct Glu Glu Glu Arg Pro Pro Arg Pro Val Cys Val Leu Asn Lys Glu Ala 290 295 300	912
cca tta cct ctt ctg caa tac aaa cgt aga cgc caa agc gag tcc aac Pro Leu Pro Leu Leu Gln Tyr Lys Arg Arg Gln Ser Glu Ser Asn 305 310 315 320	960
aac aac tca agc agg aac aca cag gac cat tgt tcg tcc aca aca aca Asn Asn Ser Ser Arg Asn Thr Gln Asp His Cys Ser Ser Thr Thr Thr 325 330 335	1008
act gtc gac aat aca acc act tta atc tca tca tct gcc gct gcc acc Thr Val Asp Asn Thr Thr Leu Ile Ser Ser Ser Ala Ala Ala Thr 340 345 350	1056
aac act gcc atc tct gca ttg ctt gag ttc tca ctc atg ggt atc tcc Asn Thr Ala Ile Ser Ala Leu Leu Glu Phe Ser Leu Met Gly Ile Ser 355 360 365	1104
gac aag aaa gaa aag ccg cag caa ccg cta cgt cct cac aag gaa cct Asp Lys Lys Glu Lys Pro Gln Gln Pro Leu Arg Pro His Lys Glu Pro 370 375 380	1152
ttg cct cca act cca ctt gca tct cct gaa gag aag gtt aat gat Leu Pro Pro Gln Thr Pro Leu Ala Ser Pro Glu Glu Lys Val Asn Asp 385 390 395 400	1200
ctc cag aag gag att cac cag atg tct gtt gaa aga gaa act ttc aag Leu Gln Lys Glu Ile His Gln Met Ser Val Glu Arg Glu Thr Phe Lys 405 410 415	1248
ctt gaa atg atg gca gaa gct atg atc agt att ctc cag tca agg Leu Glu Met Met Ser Ala Glu Ala Met Ile Ser Ile Leu Gln Ser Arg 420 425 430	1296
atc gat gcg ctg cgt cag gag aac gag gaa ctc aag aag aac aat gct Ile Asp Ala Leu Arg Gln Glu Asn Glu Leu Lys Lys Asn Asn Ala 435 440 445	1344
aat gga caa taa Asn Gly Gln 450	1356

<210> SEQ ID NO 72
<211> LENGTH: 451
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 72

Met Gly Arg Glu Ser Val Ala Val Val Thr Ala Pro Pro Ser Ala Thr 1 5 10 15
Ala Pro Gly Thr Ala Ser Val Ala Thr Ser Leu Ala Pro Gly Phe Arg 20 25 30
Phe His Pro Thr Asp Glu Glu Leu Val Ser Tyr Tyr Leu Lys Arg Lys 35 40 45
Val Leu Gly Gln Pro Val Arg Phe Asp Ala Ile Gly Glu Val Asp Ile 50 55 60
Tyr Lys His Glu Pro Trp Asp Leu Ala Val Phe Ser Arg Leu Lys Thr 65 70 75 80

Arg Asp Gln Glu Trp Tyr Phe Tyr Ser Ala Leu Asp Lys Lys Tyr Gly
 85 90 95
 Asn Gly Ala Arg Met Asn Arg Ala Thr Asn Arg Gly Tyr Trp Lys Ala
 100 105 110
 Thr Gly Lys Asp Arg Glu Ile Arg Arg Asp Ile Leu Leu Leu Gly Met
 115 120 125
 Lys Lys Thr Leu Val Phe His Ser Gly Arg Ala Pro Asp Gly Leu Arg
 130 135 140
 Thr Asn Trp Val Met His Glu Tyr Arg Leu Val Glu Tyr Glu Thr Glu
 145 150 155 160
 Lys Asn Gly Asn Leu Val Gln Asp Ala Tyr Val Leu Cys Arg Val Phe
 165 170 175
 His Lys Asn Asn Ile Gly Pro Pro Ser Gly Asn Arg Tyr Ala Pro Phe
 180 185 190
 Met Glu Glu Glu Trp Ala Asp Asp Glu Gly Ala Leu Ile Pro Gly Ile
 195 200 205
 Asp Val Lys Leu Arg Leu Glu Pro Pro Pro Val Ala Asn Gly Asn Asp
 210 215 220
 Gln Met Asp Gln Glu Ile Gln Ser Ala Ser Lys Ser Leu Ile Asn Ile
 225 230 235 240
 Asn Glu Pro Pro Arg Glu Thr Ala Pro Leu Asp Ile Glu Ser Asp Gln
 245 250 255
 Gln Asn His His Glu Asn Asp Leu Lys Pro Glu Glu His Asn Asn Asn
 260 265 270
 Asn Asn Tyr Asp Glu Asn Glu Glu Thr Leu Lys Arg Glu Gln Met Glu
 275 280 285
 Glu Glu Glu Arg Pro Pro Arg Pro Val Cys Val Leu Asn Lys Glu Ala
 290 295 300
 Pro Leu Pro Leu Leu Gln Tyr Lys Arg Arg Gln Ser Glu Ser Asn
 305 310 315 320
 Asn Asn Ser Ser Arg Asn Thr Gln Asp His Cys Ser Ser Thr Thr Thr
 325 330 335
 Thr Val Asp Asn Thr Thr Thr Leu Ile Ser Ser Ser Ala Ala Ala Thr
 340 345 350
 Asn Thr Ala Ile Ser Ala Leu Leu Glu Phe Ser Leu Met Gly Ile Ser
 355 360 365
 Asp Lys Lys Glu Lys Pro Gln Gln Pro Leu Arg Pro His Lys Glu Pro
 370 375 380
 Leu Pro Pro Gln Thr Pro Leu Ala Ser Pro Glu Glu Lys Val Asn Asp
 385 390 395 400
 Leu Gln Lys Glu Ile His Gln Met Ser Val Glu Arg Glu Thr Phe Lys
 405 410 415
 Leu Glu Met Met Ser Ala Glu Ala Met Ile Ser Ile Leu Gln Ser Arg
 420 425 430
 Ile Asp Ala Leu Arg Gln Glu Asn Glu Leu Lys Lys Asn Asn Ala
 435 440 445
 Asn Gly Gln
 450

<210> SEQ ID NO 73
 <211> LENGTH: 726
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana
 <220> FEATURE:

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<221> NAME/KEY: CDS

<222> LOCATION: (1) .. (726)

<400> SEQUENCE: 73

atg gca act aaa caa gaa gct tta gcc atc gat ttc ata agc caa cac	48
Met Ala Thr Lys Gln Glu Ala Leu Ala Ile Asp Phe Ile Ser Gln His	
1 5 10 15	
ctt ctc aca gac ttt gtt tcc atg gaa act gat cac cca tct ctt ttt	96
Leu Leu Thr Asp Phe Val Ser Met Glu Thr Asp His Pro Ser Leu Phe	
20 25 30	
acc aac caa ctt cac aac ttt cac tca gaa aca ggc cct aga acc atc	144
Thr Asn Gln Leu His Asn Phe His Ser Glu Thr Gly Pro Arg Thr Ile	
35 40 45	
acc aac caa tcc cct aaa ccg aat tcg act ctt aac cag cgt aaa ccg	192
Thr Asn Gln Ser Pro Lys Pro Asn Ser Thr Leu Asn Gln Arg Lys Pro	
50 55 60	
ccc tta ccg aat cta tcc gtc tcg aga acg gtt tca aca aag aca gag	240
Pro Leu Pro Asn Leu Ser Val Arg Thr Val Ser Thr Lys Thr Glu	
65 70 75 80	
aaa gag gaa gaa gag agg cac tac agg gga gtg aga cga aga ccg tgg	288
Lys Glu Glu Glu Arg His Tyr Arg Gly Val Arg Arg Arg Pro Trp	
85 90 95	
gga aaa tac gcg gcg gag att agg gat ccg aac aaa aag ggt tgt agg	336
Gly Lys Tyr Ala Ala Glu Ile Arg Asp Pro Asn Lys Lys Gly Cys Arg	
100 105 110	
atc tgg ctt ggg act tac gac act gcc gtg gaa gct gga aga gct tat	384
Ile Trp Leu Gly Thr Tyr Asp Thr Ala Val Glu Ala Gly Arg Ala Tyr	
115 120 125	
gac caa gcg gcg ttt caa tta cgt gga aga aaa gca atc ttg aat ttc	432
Asp Gln Ala Ala Phe Gln Leu Arg Gly Arg Lys Ala Ile Leu Asn Phe	
130 135 140	
cct ctc gat gtt agg gtt acg tca gaa act tgt tct ggg gaa gga gtt	480
Pro Leu Asp Val Arg Val Thr Ser Glu Thr Cys Ser Gly Glu Gly Val	
145 150 155 160	
atc gga tta ggg aaa cga aag cga gat aag ggt tct ccg ccg gaa gag	528
Ile Gly Leu Gly Lys Arg Lys Arg Asp Lys Gly Ser Pro Pro Glu Glu	
165 170 175	
gag aag gcg gct agg gtt aaa gtg gag gaa gaa gag agt aat acg tcg	576
Glu Lys Ala Ala Arg Val Lys Val Glu Glu Glu Ser Asn Thr Ser	
180 185 190	
gag acg acg gag gct gag gtt gag ccg gtg gta cca ttg acg ccg tca	624
Glu Thr Glu Ala Glu Val Glu Pro Val Val Pro Leu Thr Pro Ser	
195 200 205	
agt tgg atg ggg ttt tgg gat gtg gga gca gga gat ggt att ttc agt	672
Ser Trp Met Gly Phe Trp Asp Val Gly Ala Gly Asp Gly Ile Phe Ser	
210 215 220	
att cct ccg tta tct ccg acg tct ccc aac ttt tcc gtt atc tcc gtc	720
Ile Pro Pro Leu Ser Pro Thr Ser Pro Asn Phe Ser Val Ile Ser Val	
225 230 235 240	
act taa	726
Thr	

<210> SEQ_ID NO 74

<211> LENGTH: 241

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 74

Met Ala Thr Lys Gln Glu Ala Leu Ala Ile Asp Phe Ile Ser Gln His	
1 5 10 15	

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Leu Leu Thr Asp Phe Val Ser Met Glu Thr Asp His Pro Ser Leu Phe
20 25 30

Thr Asn Gln Leu His Asn Phe His Ser Glu Thr Gly Pro Arg Thr Ile
35 40 45

Thr Asn Gln Ser Pro Lys Pro Asn Ser Thr Leu Asn Gln Arg Lys Pro
50 55 60

Pro	Leu	Pro	Asn	Leu	Ser	Val	Ser	Arg	Thr	Val	Ser	Thr	Lys	Thr	Glu
65				70					75						80

Lys Glu Glu Glu Glu Arg His Tyr Arg Gly Val Arg Arg Arg Pro Trp
85 90 95

Gly Lys Tyr Ala Ala Glu Ile Arg Asp Pro Asn Lys Lys Gly Cys Arg
100 105 110

Ile Trp Leu Gly Thr Tyr Asp Thr Ala Val Glu Ala Gly Arg Ala Tyr
 115 120 125

Asp Gln Ala Ala Phe Gln Leu Arg Gly Arg Lys Ala Ile Leu Asn Phe
130 135 140

Pro	Leu	Asp	Val	Arg	Val	Thr	Ser	Glu	Thr	Cys	Ser	Gly	Glu	Gly	Val
145					150					155					160

Ile Gly Leu Gly Lys Arg Lys Arg Asp Lys Gly Ser Pro Pro Glu Glu
165 170 175

Glu Lys Ala Ala Arg Val Lys Val Glu Glu Glu Glu Ser Asn Thr Ser
180 185 190

Glu Thr Thr Glu Ala Glu Val Glu Pro Val Val Pro Leu Thr Pro Ser
195 200 205

Ser Trp Met Gly Phe Trp Asp Val Gly Ala Gly Asp Gly Ile Phe Ser
210 215 220

Ile	Pro	Pro	Leu	Ser	Pro	Thr	Ser	Pro	Asn	Phe	Ser	Val	Ile	Ser	Val
225					230					235					240

Thr

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<210> SEQ ID NO 75
<211> LENGTH: 579
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1) .. (579)
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<400> SEQUENCE: 75

atg	gtg	tct	atg	ctg	act	aat	gtt	gtc	tct	ggg	gag	acc	gaa	ccc	tcg	48
Met	Val	Ser	Met	Leu	Thr	Asn	Val	Val	Ser	Gly	Glu	Thr	Glu	Pro	Ser	
1				5					10					15		

tct ttg cct cct caa cca ttg att acc ggt tca gct gtg act aaa gaa	144	
Ser Leu Pro Pro Gln Pro Leu Ile Thr Gly Ser Ala Val Thr Lys Glu		
35	40	45
tgt gaa agc tca atg tcc ttg gag agg cca aaa aaa tat aga gga gta	192	

agg caa cga cca tgg gga aaa tgg gcg gcg gag att cga gac cca cac 240
 Arg Gln Arg Pro Trp Glv Lys Trp Ala Ala Glu Ile Arg Asp Pro His

aag gca aca cgt gta tgg ctt ggg aca ttc gag aca gcc gag gcc gcc
Lys Ala Thr Arg Val Trp Leu Gly Thr Phe Glu Thr Ala Glu Ala Ala 288

-continued

gca aga gcc tat gat gcg gca gca ctt cgc ttt aga gga agc aaa gca Ala Arg Ala Tyr Asp Ala Ala Ala Leu Arg Phe Arg Gly Ser Lys Ala 100 105 110	336
aag ctt aat ttc ccc gaa aat gtt gga act cag acg att caa cga aat Lys Leu Asn Phe Pro Glu Asn Val Gly Thr Gln Thr Ile Gln Arg Asn 115 120 125	384
tct cat ttc ttg caa aac tct atg caa cct tct ctg aca tac atc gat Ser His Phe Leu Gln Asn Ser Met Gln Pro Ser Leu Thr Tyr Ile Asp 130 135 140	432
caa tgt cca act cta tta tct tac tct cga tgt atg gag caa caa caa Gln Cys Pro Thr Leu Leu Ser Tyr Ser Arg Cys Met Glu Gln Gln Gln 145 150 155 160	480
cca tta gta ggc atg ttg cag cca aca gaa gag gaa aat cac ttt ttc Pro Leu Val Gly Met Leu Gln Pro Thr Glu Glu Glu Asn His Phe Phe 165 170 175	528
gaa aaa cca tgg acc gaa tat gat caa tac aat tac tcc tct ttt ggt Glu Lys Pro Trp Thr Glu Tyr Asp Gln Tyr Asn Tyr Ser Ser Phe Gly 180 185 190	576
taa	579

<210> SEQ ID NO 76

<211> LENGTH: 192

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 76

Met Val Ser Met Leu Thr Asn Val Val Ser Gly Glu Thr Glu Pro Ser 1 5 10 15
Ala Ser Ala Thr Trp Thr Met Gly His Lys Arg Glu Arg Glu Phe 20 25 30
Ser Leu Pro Pro Gln Pro Leu Ile Thr Gly Ser Ala Val Thr Lys Glu 35 40 45
Cys Glu Ser Ser Met Ser Leu Glu Arg Pro Lys Lys Tyr Arg Gly Val 50 55 60
Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro His 65 70 75 80
Lys Ala Thr Arg Val Trp Leu Gly Thr Phe Glu Thr Ala Glu Ala Ala 85 90 95
Ala Arg Ala Tyr Asp Ala Ala Ala Leu Arg Phe Arg Gly Ser Lys Ala 100 105 110
Lys Leu Asn Phe Pro Glu Asn Val Gly Thr Gln Thr Ile Gln Arg Asn 115 120 125
Ser His Phe Leu Gln Asn Ser Met Gln Pro Ser Leu Thr Tyr Ile Asp 130 135 140
Gln Cys Pro Thr Leu Leu Ser Tyr Ser Arg Cys Met Glu Gln Gln Gln 145 150 155 160
Pro Leu Val Gly Met Leu Gln Pro Thr Glu Glu Glu Asn His Phe Phe 165 170 175
Glu Lys Pro Trp Thr Glu Tyr Asp Gln Tyr Asn Tyr Ser Ser Phe Gly 180 185 190

<210> SEQ ID NO 77

<211> LENGTH: 1080

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)...(1080)

-continued

<400> SEQUENCE: 77

atg ata agc aag gat cca aga tcg agt tta cct cca ggg ttt cga ttt Met Ile Ser Lys Asp Pro Arg Ser Ser Leu Pro Pro Gly Phe Arg Phe 1 5 10 15	48
cat cca aca gat gaa gaa ctc att ctc cat tac cta agg aag aaa gtt His Pro Thr Asp Glu Glu Leu Ile Leu His Tyr Leu Arg Lys Lys Val 20 25 30	96
tcc tct tcc cca gtc ccg ctt tcg att atc gcc gat gtc gat atc tac Ser Ser Pro Val Pro Leu Ser Ile Ile Ala Asp Val Asp Ile Tyr 35 40 45	144
aaa tcc gat cca tgg gat tta cca gct aag gct cca ttt ggg gag aaa Lys Ser Asp Pro Trp Asp Leu Pro Ala Lys Ala Pro Phe Gly Glu Lys 50 55 60	192
gag tgg tat ttt ttc agt ccg agg gat agg aaa tat cca aac gga gca Glu Trp Tyr Phe Ser Pro Arg Asp Arg Lys Tyr Pro Asn Gly Ala 65 70 75 80	240
aga cca aac aga gca gct gcg tct gga tat tgg aaa gca acc gga aca Arg Pro Asn Arg Ala Ala Ser Gly Tyr Trp Lys Ala Thr Gly Thr 85 90 95	288
gat aaa ttg att gcg gta cca aat ggt gaa ggg ttt cat gaa aac att Asp Lys Leu Ile Ala Val Pro Asn Gly Glu Gly Phe His Glu Asn Ile 100 105 110	336
ggt ata aaa aaa gct ctt gtg ttt tat aga gga aag cct cca aaa ggt Gly Ile Lys Lys Ala Leu Val Phe Tyr Arg Gly Lys Pro Pro Lys Gly 115 120 125	384
gtt aaa acc aat tgg atc atg cat gaa tat cgt ctt gcc gat tca tta Val Lys Thr Asn Trp Ile Met His Glu Tyr Arg Leu Ala Asp Ser Leu 130 135 140	432
tct ccc aaa aga att aac tct tct agg agc ggt ggt agc gaa gtt aat Ser Pro Lys Arg Ile Asn Ser Ser Arg Ser Gly Gly Ser Glu Val Asn 145 150 155 160	480
aat aat ttt gga gat agg aat tct aaa gaa tat tcg atg aga ctg gat Asn Asn Phe Gly Asp Arg Asn Ser Lys Glu Tyr Ser Met Arg Leu Asp 165 170 175	528
gat tgg gtt ctt tgc cgg att tac aag aaa tca cac gct tca ttg tca Asp Trp Val Leu Cys Arg Ile Tyr Lys Ser His Ala Ser Leu Ser 180 185 190	576
tca cct gat gtt gct ttg gtc aca agc aat caa gag cat gag gaa aat Ser Pro Asp Val Ala Leu Val Thr Ser Asn Gln Glu His Glu Glu Asn 195 200 205	624
gac aac gaa cca ttc gta gac cgc gga acc ttt ttg cca aat ttg caa Asp Asn Glu Pro Phe Val Asp Arg Gly Thr Phe Leu Pro Asn Leu Gln 210 215 220	672
aat gat caa ccc ctt aaa cgc cag aag tct tct tgt tcg ttc tca aac Asn Asp Gln Pro Leu Lys Arg Gln Lys Ser Ser Cys Ser Phe Ser Asn 225 230 235 240	720
tta cta gac gct aca gat ttg acg ttt ctc gca aat ttt cta aac gaa Leu Leu Asp Ala Thr Asp Leu Thr Phe Leu Ala Asn Phe Leu Asn Glu 245 250 255	768
acc ccg gaa aat cgt tct gaa tca gat ttt tct ttc atg att ggc aat Thr Pro Glu Asn Arg Ser Glu Ser Asp Phe Ser Phe Met Ile Gly Asn 260 265 270	816
ttc tct aat cct gac att tac gga aac cat tac ttg gat cag aag tta Phe Ser Asn Pro Asp Ile Tyr Gly Asn His Tyr Leu Asp Gln Lys Leu 275 280 285	864
ccg cag ttg agc tct ccc act tca gag aca agc ggc atc gga agc aaa Pro Gln Leu Ser Ser Pro Thr Ser Glu Thr Ser Gly Ile Gly Ser Lys 290 295 300	912

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aga gag aga gtg gat ttt gcg gaa gaa acg ata aac gct tcg aag aag    960
Arg Glu Arg Val Asp Phe Ala Glu Glu Thr Ile Asn Ala Ser Lys Lys
305          310          315          320

```

```

atg atg aac aca tat agt tac aat aat agt ata gat caa atg gat cat    1008
Met Met Asn Thr Tyr Ser Tyr Asn Asn Ser Ile Asp Gln Met Asp His
325          330          335

```

```

agt atg atg caa caa cct agt ttc ctg aac cag gaa ctc atg atg agt    1056
Ser Met Met Gln Gln Pro Ser Phe Leu Asn Gln Glu Leu Met Met Ser
340          345          350

```

```

tct cac ctt caa tat caa ggc tag    1080
Ser His Leu Gln Tyr Gln Gly
355

```

<210> SEQ ID NO 78
<211> LENGTH: 359
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 78

```

Met Ile Ser Lys Asp Pro Arg Ser Ser Leu Pro Pro Gly Phe Arg Phe
1           5           10          15

```

```

His Pro Thr Asp Glu Glu Leu Ile Leu His Tyr Leu Arg Lys Lys Val
20          25          30

```

```

Ser Ser Ser Pro Val Pro Leu Ser Ile Ile Ala Asp Val Asp Ile Tyr
35          40          45

```

```

Lys Ser Asp Pro Trp Asp Leu Pro Ala Lys Ala Pro Phe Gly Glu Lys
50          55          60

```

```

Glu Trp Tyr Phe Phe Ser Pro Arg Asp Arg Lys Tyr Pro Asn Gly Ala
65          70          75          80

```

```

Arg Pro Asn Arg Ala Ala Ser Gly Tyr Trp Lys Ala Thr Gly Thr
85          90          95

```

```

Asp Lys Leu Ile Ala Val Pro Asn Gly Glu Gly Phe His Glu Asn Ile
100         105         110

```

```

Gly Ile Lys Lys Ala Leu Val Phe Tyr Arg Gly Lys Pro Pro Lys Gly
115         120         125

```

```

Val Lys Thr Asn Trp Ile Met His Glu Tyr Arg Leu Ala Asp Ser Leu
130         135         140

```

```

Ser Pro Lys Arg Ile Asn Ser Ser Arg Ser Gly Gly Ser Glu Val Asn
145         150         155         160

```

```

Asn Asn Phe Gly Asp Arg Asn Ser Lys Glu Tyr Ser Met Arg Leu Asp
165         170         175

```

```

Asp Trp Val Leu Cys Arg Ile Tyr Lys Lys Ser His Ala Ser Leu Ser
180         185         190

```

```

Ser Pro Asp Val Ala Leu Val Thr Ser Asn Gln Glu His Glu Glu Asn
195         200         205

```

```

Asp Asn Glu Pro Phe Val Asp Arg Gly Thr Phe Leu Pro Asn Leu Gln
210         215         220

```

```

Asn Asp Gln Pro Leu Lys Arg Gln Lys Ser Ser Cys Ser Phe Ser Asn
225         230         235         240

```

```

Leu Leu Asp Ala Thr Asp Leu Thr Phe Leu Ala Asn Phe Leu Asn Glu
245         250         255

```

```

Thr Pro Glu Asn Arg Ser Glu Ser Asp Phe Ser Phe Met Ile Gly Asn
260         265         270

```

```

Phe Ser Asn Pro Asp Ile Tyr Gly Asn His Tyr Leu Asp Gln Lys Leu
275         280         285

```

-continued

Pro Gln Leu Ser Ser Pro Thr Ser Glu Thr Ser Gly Ile Gly Ser Lys
290 295 300

Arg Glu Arg Val Asp Phe Ala Glu Glu Thr Ile Asn Ala Ser Lys Lys
305 310 315 320

Met Met Asn Thr Tyr Ser Tyr Asn Asn Ser Ile Asp Gln Met Asp His
325 330 335

Ser Met Met Gln Gln Pro Ser Phe Leu Asn Gln Glu Leu Met Met Ser
340 345 350

Ser His Leu Gln Tyr Gln Gly
355

<210> SEQ ID NO 79
<211> LENGTH: 1098
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1098)

<400> SEQUENCE: 79

atg atg tca aaa tct atg agc ata tca gtg aac gga caa tct caa gtg	48
Met Met Ser Lys Ser Met Ser Ile Ser Val Asn Gly Gln Ser Gln Val	
1 5 10 15	
cct cct ggg ttt agg ttt cat ccg acc gag gaa gag ctg ttg cag tat	96
Pro Pro Gly Phe Arg Phe His Pro Thr Glu Glu Leu Leu Gln Tyr	
20 25 30	
tat ctc cgg aag aaa gtt aat agc atc gag atc gat ctt gat gtc att	144
Tyr Leu Arg Lys Lys Val Asn Ser Ile Glu Ile Asp Leu Asp Val Ile	
35 40 45	
cgc gac gtt gat ctc aac aag ctc gag cct tgg gac att caa gag atg	192
Arg Asp Val Asp Leu Asn Lys Leu Glu Pro Trp Asp Ile Gln Glu Met	
50 55 60	
tgt aaa ata gga aca acg cca caa aac gac tgg tat ttc ttt agc cac	240
Cys Lys Ile Gly Thr Thr Pro Gln Asn Asp Trp Tyr Phe Phe Ser His	
65 70 75 80	
aag gac aaa aaa tat ccg acg gga acg aga act aac aga gcc act gcg	288
Lys Asp Lys Tyr Pro Thr Gly Thr Arg Thr Asn Arg Ala Thr Ala	
85 90 95	
gct gga ttt tgg aaa gca act ggc cgc gac aag atc ata tat agc aat	336
Ala Gly Phe Trp Lys Ala Thr Gly Arg Asp Lys Ile Ile Tyr Ser Asn	
100 105 110	
ggc cgt aga att ggg atg aga aag act ctt gtt ttc tac aaa ggc cga	384
Gly Arg Arg Ile Gly Met Arg Lys Thr Leu Val Phe Tyr Lys Gly Arg	
115 120 125	
gct cct cac ggc caa aaa tct gat tgg atc atg cat gaa tat aga ctc	432
Ala Pro His Gly Gln Lys Ser Asp Trp Ile Met His Glu Tyr Arg Leu	
130 135 140	
gat gac aac att att tcc ccc gag gat gtc acc gtt cat gag gtc gtg	480
Asp Asp Asn Ile Ile Ser Pro Glu Asp Val Thr Val His Glu Val Val	
145 150 155 160	
agt att ata ggg gaa gca tca caa gac gaa gga tgg gtg gtg tgt cgt	528
Ser Ile Ile Gly Glu Ala Ser Gln Asp Glu Gly Trp Val Val Cys Arg	
165 170 175	
att ttc aag aag aat ctt cac aaa acc cta aac agt ccc gtc gga	576
Ile Phe Lys Lys Asn Leu His Lys Thr Leu Asn Ser Pro Val Gly	
180 185 190	
gga gct tcc ctg agc ggc gga gat acg ccg aag acg aca tca tct	624
Gly Ala Ser Leu Ser Gly Gly Asp Thr Pro Lys Thr Thr Ser Ser	
195 200 205	

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cag atc ttc aac gag gat act ctc gac caa ttt ctt gaa ctt atg ggg Gln Ile Phe Asn Glu Asp Thr Leu Asp Gln Phe Leu Glu Leu Met Gly 210 215 220	672
aga tct tgt aaa gaa gag cta aat ctt gac cct ttc atg aaa ctc cca Arg Ser Cys Lys Glu Glu Leu Asn Leu Asp Pro Phe Met Lys Leu Pro 225 230 235 240	720
aac ctc gaa agc cct aac agt cag gca atc aac aac tgc cac gta agc Asn Leu Glu Ser Pro Asn Ser Gln Ala Ile Asn Asn Cys His Val Ser 245 250 255	768
tct ccc gac act aat cat aat atc cac gtc agc aac gtg gtc gac act Ser Pro Asp Thr Asn His Asn Ile His Val Ser Asn Val Val Asp Thr 260 265 270	816
agc ttt gtt act agc tgg gcc gct tta gac cgc ctc gtg gcc tcg cag Ser Phe Val Thr Ser Trp Ala Ala Leu Asp Arg Leu Val Ala Ser Gln 275 280 285	864
ctt aac gga ccc aca tca tat tca att aca gcc gtc aat gag agc cac Leu Asn Gly Pro Thr Ser Tyr Ser Ile Thr Ala Val Asn Glu Ser His 290 295 300	912
gtg ggc cat gat cat ctc gct ttg cct tcc gtc cga tct ccg tac ccc Val Gly His Asp His Leu Ala Leu Pro Ser Val Arg Ser Pro Tyr Pro 305 310 315 320	960
agc cta aac cgg tcc gct tcg tac cac gcc ggt tta aca cag gaa tat Ser Leu Asn Arg Ser Ala Ser Tyr His Ala Gly Leu Thr Gln Glu Tyr 325 330 335	1008
aca ccg gag atg gag cta tgg aat acg acg acg tcg tct cta tcg tca Thr Pro Glu Met Glu Leu Trp Asn Thr Thr Ser Ser Leu Ser Ser 340 345 350	1056
tcg cct ggc cca ttt tgt cac gtg tcg aat ggt agt gga taa Ser Pro Gly Pro Phe Cys His Val Ser Asn Gly Ser Gly 355 360 365	1098

<210> SEQ ID NO 80

<211> LENGTH: 365

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 80

Met Met Ser Lys Ser Met Ser Ile Ser Val Asn Gly Gln Ser Gln Val	
1 5 10 15	

Pro Pro Gly Phe Arg Phe His Pro Thr Glu Glu Glu Leu Leu Gln Tyr	
20 25 30	

Tyr Leu Arg Lys Lys Val Asn Ser Ile Glu Ile Asp Leu Asp Val Ile	
35 40 45	

Arg Asp Val Asp Leu Asn Lys Leu Glu Pro Trp Asp Ile Gln Glu Met	
50 55 60	

Cys Lys Ile Gly Thr Thr Pro Gln Asn Asp Trp Tyr Phe Phe Ser His	
65 70 75 80	

Lys Asp Lys Lys Tyr Pro Thr Gly Thr Arg Thr Asn Arg Ala Thr Ala	
85 90 95	

Ala Gly Phe Trp Lys Ala Thr Gly Arg Asp Lys Ile Ile Tyr Ser Asn	
100 105 110	

Gly Arg Arg Ile Gly Met Arg Lys Thr Leu Val Phe Tyr Lys Gly Arg	
115 120 125	

Ala Pro His Gly Gln Lys Ser Asp Trp Ile Met His Glu Tyr Arg Leu	
130 135 140	

Asp Asp Asn Ile Ile Ser Pro Glu Asp Val Thr Val His Glu Val Val	
145 150 155 160	

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Ser Ile Ile Gly Glu Ala Ser Gln Asp Glu Gly Trp Val Val Cys Arg
165 170 175

Ile Phe Lys Lys Lys Asn Leu His Lys Thr Leu Asn Ser Pro Val Gly
180 185 190

Gly Ala Ser Leu Ser Gly Gly Asp Thr Pro Lys Thr Thr Ser Ser
195 200 205

Gln Ile Phe Asn Glu Asp Thr Leu Asp Gln Phe Leu Glu Leu Met Gly
210 215 220

Arg Ser Cys Lys Glu Glu Leu Asn Leu Asp Pro Phe Met Lys Leu Pro
225 230 235 240

Asn Leu Glu Ser Pro Asn Ser Gln Ala Ile Asn Asn Cys His Val Ser
245 250 255

Ser Pro Asp Thr Asn His Asn Ile His Val Ser Asn Val Val Asp Thr
260 265 270

Ser Phe Val Thr Ser Trp Ala Ala Leu Asp Arg Leu Val Ala Ser Gln
275 280 285

Leu Asn Gly Pro Thr Ser Tyr Ser Ile Thr Ala Val Asn Glu Ser His
290 295 300

Val Gly His Asp His Leu Ala Leu Pro Ser Val Arg Ser Pro Tyr Pro
305 310 315 320

Ser Leu Asn Arg Ser Ala Ser Tyr His Ala Gly Leu Thr Gln Glu Tyr
325 330 335

Thr Pro Glu Met Glu Leu Trp Asn Thr Thr Ser Ser Leu Ser Ser
340 345 350

Ser Pro Gly Pro Phe Cys His Val Ser Asn Gly Ser Gly
355 360 365

<210> SEQ ID NO: 81
<211> LENGTH: 777
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(777)

<400> SEQUENCE: 81

atg gga aag aga gca act act agt gtg agg aga gaa gag tta aac aga Met Gly Lys Arg Ala Thr Thr Ser Val Arg Arg Glu Glu Leu Asn Arg	48
1 5 10 15	
gga gct tgg act gat cat gaa gac aag atc ctt aga gat tac atc acc Gly Ala Trp Thr Asp His Glu Asp Lys Ile Leu Arg Asp Tyr Ile Thr	96
20 25 30	
act cac ggc gaa ggc aaa tgg agc act ctc cct aac caa gct ggt ctc Thr His Gly Glu Gly Lys Trp Ser Thr Leu Pro Asn Gln Ala Gly Leu	144
35 40 45	
aag agg tgt ggc aaa agc tgt aga ctt cgg tgg aag aac tac cta aga Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Lys Asn Tyr Leu Arg	192
50 55 60	
ccg ggg ata aag cgc ggt aac atc tca tct gat gaa gaa gaa ctc ata Pro Gly Ile Lys Arg Gly Asn Ile Ser Ser Asp Glu Glu Leu Ile	240
65 70 75 80	
atc cgt ctc cat aat ctt ctt gga aac aga tgg tcg ttg ata gct ggg Ile Arg Leu His Asn Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly	288
85 90 95	
agg ctt cca ggc cga aca gac aat gaa ata aag aat cat tgg aac tca Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn His Trp Asn Ser	336
100 105 110	

-continued

aac ctc cgc aaa aga ctt ccc aaa act caa acc aag caa cca aaa cgt Asn Leu Arg Lys Arg Leu Pro Lys Thr Gln Thr Lys Gln Pro Lys Arg 115 120 125	384
ata aaa cat tcg acg aac aac gag aat aat gta tgt gtt ata cgt aca Ile Lys His Ser Thr Asn Asn Glu Asn Asn Val Cys Val Ile Arg Thr 130 135 140	432
aag gcg att agg tgc tca aag act ctt ctc ttc tcg gat ctc tct ctt Lys Ala Ile Arg Cys Ser Lys Thr Leu Leu Phe Ser Asp Leu Ser Leu 145 150 155 160	480
cag aag aag agt act agt cca cta cct ctg aaa gaa caa gag atg Gln Lys Ser Ser Thr Ser Pro Leu Pro Leu Lys Glu Gln Glu Met 165 170 175	528
gat caa ggt gga tct tcg ttg atg gga gat ctc gaa ttc gat ttc gat Asp Gln Gly Gly Ser Ser Leu Met Gly Asp Leu Glu Phe Asp Phe Asp 180 185 190	576
agg atc cat tcg gag ttt cac ttc ccg gat ttg atg gat ttt gat ggt Arg Ile His Ser Glu Phe His Phe Pro Asp Leu Met Asp Phe Asp Gly 195 200 205	624
ttg gac tgt gga aac gtt aca tct ctt gtt tca tct aac gag att ttg Leu Asp Cys Gly Asn Val Thr Ser Leu Val Ser Ser Asn Glu Ile Leu 210 215 220	672
gga gag ttg cct gct caa ggt aat ctc gat ctc aat aga cct ttc Gly Glu Leu Val Pro Ala Gln Gly Asn Leu Asp Leu Asn Arg Pro Phe 225 230 235 240	720
act tct tgt cat cat cgt ggc gac gat gaa gat tgg ctc cga gac ttc Thr Ser Cys His His Arg Gly Asp Asp Glu Asp Trp Leu Arg Asp Phe 245 250 255	768
act tgt tga Thr Cys	777
<210> SEQ ID NO: 82 <211> LENGTH: 258 <212> TYPE: PRT <213> ORGANISM: Arabidopsis thaliana	
<400> SEQUENCE: 82	
Met Gly Lys Arg Ala Thr Thr Ser Val Arg Arg Glu Glu Leu Asn Arg 1 5 10 15	
Gly Ala Trp Thr Asp His Glu Asp Lys Ile Leu Arg Asp Tyr Ile Thr 20 25 30	
Thr His Gly Glu Gly Lys Trp Ser Thr Leu Pro Asn Gln Ala Gly Leu 35 40 45	
Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Lys Asn Tyr Leu Arg 50 55 60	
Pro Gly Ile Lys Arg Gly Asn Ile Ser Ser Asp Glu Glu Leu Ile 65 70 75 80	
Ile Arg Leu His Asn Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly 85 90 95	
Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn His Trp Asn Ser 100 105 110	
Asn Leu Arg Lys Arg Leu Pro Lys Thr Gln Thr Lys Gln Pro Lys Arg 115 120 125	
Ile Lys His Ser Thr Asn Asn Glu Asn Asn Val Cys Val Ile Arg Thr 130 135 140	
Lys Ala Ile Arg Cys Ser Lys Thr Leu Leu Phe Ser Asp Leu Ser Leu 145 150 155 160	
Gln Lys Lys Ser Ser Thr Ser Pro Leu Pro Leu Lys Glu Gln Glu Met 165 170 175	

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Asp Gln Gly Gly Ser Ser Leu Met Gly Asp Leu Glu Phe Asp Phe Asp
 180 185 190

Arg Ile His Ser Glu Phe His Phe Pro Asp Leu Met Asp Phe Asp Gly
 195 200 205

Leu Asp Cys Gly Asn Val Thr Ser Leu Val Ser Ser Asn Glu Ile Leu
 210 215 220

Gly Glu Leu Val Pro Ala Gln Gly Asn Leu Asp Leu Asn Arg Pro Phe
 225 230 235 240

Thr Ser Cys His His Arg Gly Asp Asp Glu Asp Trp Leu Arg Asp Phe
 245 250 255

Thr Cys

<210> SEQ_ID NO 83
 <211> LENGTH: 573
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1) .. (573)

<400> SEQUENCE: 83

atg gcg ttc gca gga aca acc cag aaa tgc atg gca tgt gac aaa aca	48
Met Ala Gly Thr Thr Gln Lys Cys Met Ala Cys Asp Lys Thr	
1 5 10 15	
gtt tat ctt gtc gac aag tta acc gcc gat aac cgg gtc tac cac aaa	96
Val Tyr Leu Val Asp Lys Leu Thr Ala Asp Asn Arg Val Tyr His Lys	
20 25 30	
gct tgt ttc cga tgt cac cat tgc aaa gga act ctc aag ctt agc aat	144
Ala Cys Phe Arg Cys His His Cys Lys Gly Thr Leu Lys Leu Ser Asn	
35 40 45	
tac aac tcc ttt gaa gga gtt ctc tac tgc aga cca cat ttc gat caa	192
Tyr Asn Ser Phe Glu Gly Val Leu Tyr Cys Arg Pro His Phe Asp Gln	
50 55 60	
aac ttc aag aga act gga agt ctt gag aaa agg ttc gaa ggg aca cca	240
Asn Phe Lys Arg Thr Gly Ser Leu Glu Lys Ser Phe Glu Gly Thr Pro	
65 70 75 80	
aag att ggg aaa cct gat agg cct ttg gag gga gag aca cct gct gga	288
Lys Ile Gly Lys Pro Asp Arg Pro Leu Glu Gly Glu Arg Pro Ala Gly	
85 90 95	
acc aaa gtt tcg aat atg ttt ggt gga aca cga gag aaa tgc gtt ggt	336
Thr Lys Val Ser Asn Met Phe Gly Gly Thr Arg Glu Lys Cys Val Gly	
100 105 110	
tgc gac aaa acc gtg tat cca att gag aag gta tcg gtg aat gga aca	384
Cys Asp Lys Thr Val Tyr Pro Ile Glu Lys Val Ser Val Asn Gly Thr	
115 120 125	
ttg tac cac aag agc tgc ttc aag tgt aca cat gga ggc tgc acg ata	432
Leu Tyr His Lys Ser Cys Phe Lys Cys Thr His Gly Gly Cys Thr Ile	
130 135 140	
agc cct tcg aat tac ata gct cac gag ggt aag cta tat tgc aag cat	480
Ser Pro Ser Asn Tyr Ile Ala His Glu Gly Lys Leu Tyr Cys Lys His	
145 150 155 160	
cat cat att cag ctg atc aag gag aaa gga aac ttg agc cag ctc gaa	528
His His Ile Gln Leu Ile Lys Glu Lys Gly Asn Leu Ser Gln Leu Glu	
165 170 175	
gga gga gga gag aat gcc gcc aag gac aaa gtc gtc gct gct taa	573
Gly Gly Gly Glu Asn Ala Ala Lys Asp Lys Val Val Ala Ala	
180 185 190	

<210> SEQ_ID NO 84

-continued

<211> LENGTH: 190
 <212> TYPE: PRT
 <213> ORGANISM: Arabidopsis thaliana
 <400> SEQUENCE: 84

```

Met Ala Phe Ala Gly Thr Thr Gln Lys Cys Met Ala Cys Asp Lys Thr
1           5          10          15

Val Tyr Leu Val Asp Lys Leu Thr Ala Asp Asn Arg Val Tyr His Lys
20          25          30

Ala Cys Phe Arg Cys His His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35          40          45

Tyr Asn Ser Phe Glu Gly Val Leu Tyr Cys Arg Pro His Phe Asp Gln
50          55          60

Asn Phe Lys Arg Thr Gly Ser Leu Glu Lys Ser Phe Glu Gly Thr Pro
65          70          75          80

Lys Ile Gly Lys Pro Asp Arg Pro Leu Glu Gly Glu Arg Pro Ala Gly
85          90          95

Thr Lys Val Ser Asn Met Phe Gly Gly Thr Arg Glu Lys Cys Val Gly
100         105         110

Cys Asp Lys Thr Val Tyr Pro Ile Glu Lys Val Ser Val Asn Gly Thr
115         120         125

Leu Tyr His Lys Ser Cys Phe Lys Cys Thr His Gly Gly Cys Thr Ile
130         135         140

Ser Pro Ser Asn Tyr Ile Ala His Glu Gly Lys Leu Tyr Cys Lys His
145         150         155         160

His His Ile Gln Leu Ile Lys Glu Lys Gly Asn Leu Ser Gln Leu Glu
165         170         175

Gly Gly Gly Glu Asn Ala Ala Lys Asp Lys Val Val Ala Ala
180         185         190
  
```

<210> SEQ ID NO 85
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 85

gatgggtta gctactacaa cttttctat 30

<210> SEQ ID NO 86
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 86

aaaatctcca aagtctctaa cggagaaaaga 30

<210> SEQ ID NO 87
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 87

gatggccgct gaggatcgaa gtgaggaact 30

-continued

<210> SEQ ID NO 88
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 88

gcatatacgt gcttttggc ttttttttc

30

<210> SEQ ID NO 89
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 89

gatggctgct ttttcattttt ccgctgcttc

30

<210> SEQ ID NO 90
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 90

gaaaactcgca tggatggattc cataagggtgg

30

<210> SEQ ID NO 91
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 91

aatggaaaaa gccttgagaa acttc

25

<210> SEQ ID NO 92
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 92

tccccacgat cttcggcaag taca

24

<210> SEQ ID NO 93
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 93

gatggaaagt ctgcacaca ttccctcccg

30

<210> SEQ ID NO 94
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

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<400> SEQUENCE: 94

cgtgtgtgta ttttgagccc aagagtagaa

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<210> SEQ ID NO 95
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 95

atggaagccg agaagaaaaat gg

22

<210> SEQ ID NO 96
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 96

aacagctaaa agaggatccg ac

22

<210> SEQ ID NO 97
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 97

atggcgatt cgtttccga c

21

<210> SEQ ID NO 98
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 98

ggaaaaatgt ttccaagatt cg

22

<210> SEQ ID NO 99
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 99

atggaagaag caatcatgag ac

22

<210> SEQ ID NO 100
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 100

ataatcatca tgaaagcaat actg

24

<210> SEQ ID NO 101
<211> LENGTH: 30

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 101

gatgtcaaga aagccatgtt gtgtgggaga

30

<210> SEQ ID NO 102
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 102

tatgaaggtc ttgtcgctgt aatcttggct

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<210> SEQ ID NO 103
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 103

gatggctcgt ggaaagattc agcttaagag

30

<210> SEQ ID NO 104
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 104

gaactgaaat attcacttg gcattgttag

30

<210> SEQ ID NO 105
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 105

gatggcaatg tcttgcaagg atggtaagtt

30

<210> SEQ ID NO 106
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 106

cacaaaaggac caattgatga acacaaaagca

30

<210> SEQ ID NO 107
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 107

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atggctgaac gaaagaaaacg c

21

<210> SEQ ID NO 108
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 108

tgggcacgca atattaagag g

21

<210> SEQ ID NO 109
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 109

gatggggaga cattttgct gttacaaaca

30

<210> SEQ ID NO 110
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 110

aaggactga caaaaagaga cggccattct

30

<210> SEQ ID NO 111
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 111

gatggccgat gaggtcacaa tcgggtttcg

30

<210> SEQ ID NO 112
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 112

aggccaagtc agctgttccc agtccccat

30

<210> SEQ ID NO 113
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 113

atggcaagac aaatcaacat agag

24

<210> SEQ ID NO 114
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 114

ttcagataga aaaaacggct cttc

24

<210> SEQ ID NO 115
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 115

atgggtcatgg agcccaagaa g

21

<210> SEQ ID NO 116
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 116

tgaaccattt tcctctgcac tc

22

<210> SEQ ID NO 117
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 117

atgagatcag gagaatgtga tg

22

<210> SEQ ID NO 118
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 118

agaatctgat tcattatcgc tac

23

<210> SEQ ID NO 119
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 119

gatggaaag agagcaacta ctagtgtgag

30

<210> SEQ ID NO 120
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 120

acaagtgaag tctcgagcc aatcttcatc

30

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<210> SEQ ID NO 121
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 121

gatgaagtca agacgtgaac aatcaatcg

30

<210> SEQ ID NO 122
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 122

tttatagtaa cctcgaatgt gctggggcaa

30

<210> SEQ ID NO 123
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 123

gatgtctggt tcgaccggaa aagaaaatggaa

30

<210> SEQ ID NO 124
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 124

ctcgatcccta cctaattccaa taaaactctct

30

<210> SEQ ID NO 125
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 125

gatggagggtg gagaagagggaa ttgttag

26

<210> SEQ ID NO 126
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 126

ctcatcagct gaggttaggag gag

23

<210> SEQ ID NO 127
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

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<400> SEQUENCE: 127

gatggagttg gagcctataat catcgagttg

30

<210> SEQ ID NO 128

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 128

tccgacctgc atccgacattt gacggccatg

30

<210> SEQ ID NO 129

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 129

gatggaggtt atgagaccgt cgacgtcaca

30

<210> SEQ ID NO 130

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 130

tagttgaaac atttgtttt gggcgtcata

30

<210> SEQ ID NO 131

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 131

atggcgaggtt ttgaggaaag c

21

<210> SEQ ID NO 132

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 132

aaatgcata caggaagatg aag

23

<210> SEQ ID NO 133

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 133

gatgataaggc aaggatccaa gatcgagt

30

<210> SEQ ID NO 134

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<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 134

gccttgatat tgaaggtagag aactcatcat

30

<210> SEQ ID NO 135
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 135

gatggagggt ggtgcgagta atgaagttagc

30

<210> SEQ ID NO 136
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 136

aacaagttgc agaggtgggtt ggtcttgggtt

30

<210> SEQ ID NO 137
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 137

atggaaactg cttcttttc tttc

24

<210> SEQ ID NO 138
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 138

agaattggcc agtttactaa ttgc

24

<210> SEQ ID NO 139
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 139

atggcacgac cacaacaacgc c

21

<210> SEQ ID NO 140
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 140

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cagcgtctga gttggtaaaa cag 23

<210> SEQ ID NO 141
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 141

gatggaaaa tcttcaagct cggaggaaag 30

<210> SEQ ID NO 142
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 142

tgatagattc aaagcattat tattatgatc 30

<210> SEQ ID NO 143
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 143

gatggctgat aggatcaaag gtccatggag 30

<210> SEQ ID NO 144
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 144

ctcgattctc ccaactccaa tttgactcat 30

<210> SEQ ID NO 145
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 145

atggactttg acgaggagct aaatc 25

<210> SEQ ID NO 146
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 146

aaagaaaaggc ctcataaggac aag 23

<210> SEQ ID NO 147
<211> LENGTH: 30
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 147

gatgggtaga gggaaagatag agataaagaa

30

<210> SEQ ID NO 148
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 148

atcattctgg gccgttggat cgttttgaag

30

<210> SEQ ID NO 149
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 149

gatggaaagta acttcccaat ctaccctccc

30

<210> SEQ ID NO 150
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 150

aaacttaaac atcgcttgac gatgatggtt

30

<210> SEQ ID NO 151
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 151

atgattggag atctaatacaa g

21

<210> SEQ ID NO 152
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 152

gttcttgccct ttacccttat g

21

<210> SEQ ID NO 153
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 153

atggcacaga cgaagaagtt cag

23

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<210> SEQ ID NO 154
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 154

gtttgtattg agaagctcct ctatc

25

<210> SEQ ID NO 155
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 155

gatggactgc aacatggtat cttcgttccc

30

<210> SEQ ID NO 156
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 156

gatgaaatga ctagggaaag tgccaaatat

30

<210> SEQ ID NO 157
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 157

gatggcagct gctatgaatt tgtac

25

<210> SEQ ID NO 158
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 158

agctagaatc gaatcccaat cg

22

<210> SEQ ID NO 159
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 159

atggtaacatt cgaagaagtt ccg

23

<210> SEQ ID NO 160
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 160

gacctgtgca atggatccag

20

<210> SEQ ID NO 161

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 161

gatgggtggaa gaaggcggcg tag

23

<210> SEQ ID NO 162

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 162

gctagtatat aaatcttccc agaag

25

<210> SEQ ID NO 163

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 163

atgggtaaaa cacttcaaaa gacac

25

<210> SEQ ID NO 164

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 164

gcagaaggtc cataatctga tatc

24

<210> SEQ ID NO 165

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 165

gatggggagct ccaaagctga agtggacacc

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<210> SEQ ID NO 166

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 166

ccgagtttgg ctatgcattc tataacttcac

30

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<210> SEQ ID NO 167
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 167

gatgagttac acgagcactg acagtgcacca

30

<210> SEQ ID NO 168
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 168

acaaaactatt tcaagtgtatg gtaagggtgaa

30

<210> SEQ ID NO 169
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 169

gatggccgac ggttagtacta gttcttcgga

30

<210> SEQ ID NO 170
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 170

agcgactcca atcgtgttga atgctggatg

30

<210> SEQ ID NO 171
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 171

gatgataagc aaggatccaa gatcgagttt

30

<210> SEQ ID NO 172
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 172

ctagccttga tattgaaggt gagaactcat

30

<210> SEQ ID NO 173
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

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<400> SEQUENCE: 173

gatgatgtca aaatctatga gcatatac

27

<210> SEQ ID NO 174
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 174

ttatccacta ccattcgaca cgtgacaaaa

30

<210> SEQ ID NO 175
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 175

gggatggaa agagagcaac tactagtgtg agg

33

<210> SEQ ID NO 176
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 176

tcaacaagtg aagtctcgga gccaatcttc

30

<210> SEQ ID NO 177
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 177

gatgaacaaa acccgcccttc gtgctcttc

30

<210> SEQ ID NO 178
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 178

tcatcgaaat agaagaagcg ttttttgacc

30

<210> SEQ ID NO 179
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 179

atgagctcat ctgattccgt taataaac

27

<210> SEQ ID NO 180
<211> LENGTH: 26

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 180

ttatatccga ttatcagaat aagaac

26

<210> SEQ ID NO 181
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 181

atgaaataca gaggcgtacg aaag

24

<210> SEQ ID NO 182
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 182

gcccctttgcg tcgttacaat tg

22

<210> SEQ ID NO 183
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 183

gatggtgccg acaccgtgtt gcaaagctga

30

<210> SEQ ID NO 184
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 184

tccaaaatag ttatcaattt cgtcaaacaa

30

<210> SEQ ID NO 185
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 185

gatggagacg acgtatgaaga agaaaggag

30

<210> SEQ ID NO 186
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 186

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aatcacatgg tggtcaccat taagcaagtg

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<210> SEQ ID NO 187
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 187

atggcttctt cacatcaaca acag

24

<210> SEQ ID NO 188
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 188

agtaactacg agttgagagt gtc

23

<210> SEQ ID NO 189
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 189

atgcattatc ctaacaacag aacc

24

<210> SEQ ID NO 190
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 190

ctggaacata tcagcaattt tatttc

26

<210> SEQ ID NO 191
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 191

gatggacacg aaggcggttg gagtttc

27

<210> SEQ ID NO 192
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 192

ttctagataa aacaacattt ctatc

25

<210> SEQ ID NO 193
<211> LENGTH: 24
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<220> FEATURE:
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<400> SEQUENCE: 193

gatggagaat ccgggtgggtt taag

24

<210> SEQ ID NO 194
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 194

tgttcttgag atagaagaac attgg

25

<210> SEQ ID NO 195
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 195

atggattcga aaaaatggaat taac

24

<210> SEQ ID NO 196
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
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<400> SEQUENCE: 196

aactgtgggtt gtggctgttg ttg

23

<210> SEQ ID NO 197
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 <212> TYPE: DNA
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 <220> FEATURE:
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<400> SEQUENCE: 197

gatggattac aaggtatcaa gaag

24

<210> SEQ ID NO 198
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 <212> TYPE: DNA
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 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 198

gaatttccaa acgcaatcaa gattc

25

<210> SEQ ID NO 199
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 <212> TYPE: DNA
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 <220> FEATURE:
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<400> SEQUENCE: 199

atgaatatcg tctcttgaa agatg

25

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<210> SEQ ID NO 200
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 200

tcacatatgg tgatcacttc ctctacttg

29

<210> SEQ ID NO 201
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 201

gatggcgctcg gtgtcgctgt c

21

<210> SEQ ID NO 202
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 202

tttcttttgt gggaggttagc tg

22

<210> SEQ ID NO 203
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 203

atgatcaagg ttcaaaaaaaa gaac

24

<210> SEQ ID NO 204
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 204

taaaaaactta tcgatccaat cagtag

26

<210> SEQ ID NO 205
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 205

atggaagaaa gcaatgatata ttttc

25

<210> SEQ ID NO 206
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

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<400> SEQUENCE: 206

atggcaaga acttcccaa tcag

24

<210> SEQ ID NO 207
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 207

atggagagct caaacaggag c

21

<210> SEQ ID NO 208
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 208

tctcttcctt tcttctgaat caag

24

<210> SEQ ID NO 209
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 209

gatggaggat caagttgggt ttggg

25

<210> SEQ ID NO 210
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 210

accaacaaga atgatccaac taatg

25

<210> SEQ ID NO 211
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 211

atggacgaat atattgattt ccgac

25

<210> SEQ ID NO 212
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 212

agcaactaat agatctgata tcaatg

26

<210> SEQ ID NO 213

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<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 213

atggcggtc tcttcgggtgg

20

<210> SEQ ID NO 214
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 214

cgataaaaatt gaagcccaat ctatc

25

<210> SEQ ID NO 215
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 215

gatgatgaag gttgatcaag attattcgtg

30

<210> SEQ ID NO 216
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 216

gtcttctcca ctcataaaaa attgagacgc

30

<210> SEQ ID NO 217
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 217

atgaaaagcc gagtgagaaaa atc

23

<210> SEQ ID NO 218
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 218

ttacttatcc aacaaatgat cttgg

25

<210> SEQ ID NO 219
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 219

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gatgactcgt ccatgttctc actgcaatca	30
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<210> SEQ ID NO 220
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<220> FEATURE:
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<400> SEQUENCE: 220

ttaaggcggt atcacgttt tggatgtctga	30
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<210> SEQ ID NO 221
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 221

gatgaacaaa accccgccttc gtgtctctca	30
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<210> SEQ ID NO 222
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 222

tccggaaataga agaaggcggtt cttggacctgt	30
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<210> SEQ ID NO 223
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 223

gatggggaaat cagaagctca aatggacggc	30
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<210> SEQ ID NO 224
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 224

attcaaggtagataatctttc cctgactaca	30
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<210> SEQ ID NO 225
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 225

gatggatcca ttttaattc agtccccatt	30
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<210> SEQ ID NO 226
<211> LENGTH: 30
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 226

ccaaagtccca ctatttcag aagaccccaa                                30

<210> SEQ ID NO 227
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 227

gatggagcca atggaatctt gtacgttcc                                30

<210> SEQ ID NO 228
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 228

attatcaaat acgcaaatcc caatatcata                                30

<210> SEQ ID NO 229
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 229

atggaataa aaaaagaaga tcag                                24

<210> SEQ ID NO 230
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 230

ctcgatatgg tctggtgtg ag                                22

<210> SEQ ID NO 231
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 231

atggaaaaca gctacaccgt tg                                22

<210> SEQ ID NO 232
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 232

cttccttagac aacaacccta aac                                23

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<210> SEQ ID NO 233
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 233

gatggcggat tcttcacccg attcg

25

<210> SEQ ID NO 234
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 234

gtctttcaag agaagacttc tacc

24

<210> SEQ ID NO 235
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 235

atgtgtgggg gagctatcat ttc

23

<210> SEQ ID NO 236
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 236

attggagtct tgatagctcc

20

<210> SEQ ID NO 237
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 237

atggataatt cagaaaatgt tc

22

<210> SEQ ID NO 238
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 238

tctccaccgc cggttaattc

20

<210> SEQ ID NO 239
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 239

atgatgtatgg atgagtttat ggatc

25

<210> SEQ ID NO 240

<211> LENGTH: 22

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 240

cacaaggtaag agatcgatca tc

22

<210> SEQ ID NO 241

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 241

ggggatggcg actcctaaccg aagt

24

<210> SEQ ID NO 242

<211> LENGTH: 29

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 242

aacaacggtc aactggaaat aaccaaaccg

29

<210> SEQ ID NO 243

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 243

gatgggtagg cctccttgtt gtgacaaagg

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<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 244

gaagaaaatta gtgtttcat ccaatagaat

30

<210> SEQ ID NO 245

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 245

gatggagact ctgcattccat tctctcacct

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<210> SEQ ID NO 246
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 246
agctccggca ctgaagacat tttctccggc                                30

<210> SEQ ID NO 247
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 247
gatggatttg ctcctgggtt ttag                                24

<210> SEQ ID NO 248
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 248
gtaattccag aaagggttcaa gatc                                24

<210> SEQ ID NO 249
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 249
atgtcggtctg tgtctgaatc g                                21

<210> SEQ ID NO 250
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 250
aaccaaaccg agaggcggtg                                20

<210> SEQ ID NO 251
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 251
gatgacgggg aagcgatcaa agac                                24

<210> SEQ ID NO 252
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

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<400> SEQUENCE: 252

ggggatataa tagtcgctta gatttc

26

<210> SEQ ID NO 253
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 253

gatgatgaaa tctggggctg atttgc

26

<210> SEQ ID NO 254
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 254

gaaaagttccc tgcctaacca caagtgg

27

<210> SEQ ID NO 255
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 255

gatgaaagaa gacatggaag tactatac

27

<210> SEQ ID NO 256
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 256

tgcgactaga ctgcagaccg acatc

25

<210> SEQ ID NO 257
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 257

gatgaagtgcg gagctaaatt taccagctgg

30

<210> SEQ ID NO 258
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 258

ccccctgtgga gcaaaaactcc aattcaagaa

30

<210> SEQ ID NO 259
<211> LENGTH: 21

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 259

atgtcgtctt ccaccaatga c

21

<210> SEQ ID NO 260
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 260

gtttacaaa gagtcttgaa tcc

23

<210> SEQ ID NO 261
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 261

gatgggttg aaagatattg ggtcc

25

<210> SEQ ID NO 262
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 262

ttggaaagcg aggatattt cggtc

25

<210> SEQ ID NO 263
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 263

atgaacacaa catcatcaaa gagc

24

<210> SEQ ID NO 264
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 264

ggagccaaag tagtgaaac ct tg

24

<210> SEQ ID NO 265
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 265

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gatgaatcta ccacccggat ttagg

25

<210> SEQ ID NO 266
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 266

cggttaagctt acttcgtcaa gatc

24

<210> SEQ ID NO 267
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 267

atgcatacg ggaagagacc tc

22

<210> SEQ ID NO 268
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 268

tttcgtcgt ttgtggatac taatg

25

<210> SEQ ID NO 269
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 269

gatgaagaga gatcatcatc atcatcatca

30

<210> SEQ ID NO 270
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 270

atggcgagaa tcggatgaag c

21

<210> SEQ ID NO 271
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 271

gatggagacg gaagaagaga tgaag

25

<210> SEQ ID NO 272
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 272
gcaattccaa acagtgcctt gaatac                                26

<210> SEQ ID NO 273
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 273
atgggttttg ctctgatcca cc                                22

<210> SEQ ID NO 274
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 274
aaagacttag tagaaggctg tag                                23

<210> SEQ ID NO 275
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 275
gatgggtgca ccaaaggcaga agtggacacc                                30

<210> SEQ ID NO 276
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 276
ccaaggatga ttacggatcc tgaacttcaa                                30

<210> SEQ ID NO 277
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 277
gatggataat tcagctccag attcgttatc                                30

<210> SEQ ID NO 278
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 278
aactctaagg agctgcattt tgtagcaaa                                30

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<210> SEQ ID NO 279
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 279

atgattggag atctaatgaa g

21

<210> SEQ ID NO 280
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 280

gagactgata accggacacg

20

<210> SEQ ID NO 281
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 281

gatgaagaga gatcatcatc atcatcatca

30

<210> SEQ ID NO 282
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 282

tcaaggaatga tgactggtgc ttcc

24

<210> SEQ ID NO 283
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 283

atgggtctccg ctctcagccg

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<210> SEQ ID NO 284
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 284

ttattctctt gggttagttat aataattg

28

<210> SEQ ID NO 285
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

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<400> SEQUENCE: 285

atgagatcg gagaatgtga tg

22

<210> SEQ ID NO 286

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 286

agaatctgat tcattatcgac tac

23

<210> SEQ ID NO 287

<211> LENGTH: 26

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 287

ggggatgtac ggacagtgcataatag

26

<210> SEQ ID NO 288

<211> LENGTH: 29

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 288

gggttatgaaa ccaataactc atcaaacacg

29

<210> SEQ ID NO 289

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 289

gatgaattcg ttttcacaag tacccctgg

30

<210> SEQ ID NO 290

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 290

gagatcaatc tgacaacttg aagaagttaga

30

<210> SEQ ID NO 291

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 291

atggtctccg ctctcagccg

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<210> SEQ ID NO 292

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 292

ttctcttggg tagtgtataat aatttg

25

<210> SEQ ID NO 293
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 293

atgaaacgaa ttgttcgaat ttcattc

27

<210> SEQ ID NO 294
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 294

aacaaacttct tcagaaggcac cac

23

<210> SEQ ID NO 295
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 295

gatggggaaa actcaactcg ctccctggatt

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<210> SEQ ID NO 296
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 296

catttttgggt ctatgtctca tggaaggcaga

30

<210> SEQ ID NO 297
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 297

gggatggcgt tcgcaggaac aaccaggaaa tg

32

<210> SEQ ID NO 298
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 298

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agcagcgacg actttgtcct tggcg 25

<210> SEQ ID NO 299
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 299

gatggaaaac atggggatt cgagcatag 29

<210> SEQ ID NO 300
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 300

tgagtgcac agtcatgttag gaagctg 27

<210> SEQ ID NO 301
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 301

atggagggtt acgaagacat tg 22

<210> SEQ ID NO 302
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 302

tccctttcc ttgccttgt c 21

<210> SEQ ID NO 303
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 303

atgagaatga caagagatgg aaaag 25

<210> SEQ ID NO 304
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 304

aaggcaatac ccattagtaa aatccatcat ag 32

<210> SEQ ID NO 305
<211> LENGTH: 30
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 305

gatggataat gtcaaacttg ttaagaatgg

30

<210> SEQ ID NO 306
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 306

tctgaaacta ttgcaactac tggctcttc

30

<210> SEQ ID NO 307
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 307

gatggagagt acagattctt ccgggtgtcc

30

<210> SEQ ID NO 308
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 308

agaataccaa ttcaaaccag gcaattggta

30

<210> SEQ ID NO 309
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 309

atggcttttg gcaatatcca ag

22

<210> SEQ ID NO 310
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 310

aaaagaagat aataacgtct cc

22

<210> SEQ ID NO 311
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 311

atggcgagtt ttgaggaaag c

21

<210> SEQ ID NO 312
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 312

aatatgcata caggaagatg aag

23

<210> SEQ ID NO 313
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 313

atgggtgaagc aaggcgtgaa gg

22

<210> SEQ ID NO 314
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 314

aaaatcccaa agaatcaaag attc

24

<210> SEQ ID NO 315
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 315

gatggaatcg gtggatcaat catgttagtgc

30

<210> SEQ ID NO 316
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 316

aacatgtaaa tcccttatata agtcatagtc

30

<210> SEQ ID NO 317
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 317

atgaacaaca acatttcag tactac

26

<210> SEQ ID NO 318
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 318

actgtgtata gctttagata aaacc

25

<210> SEQ ID NO 319

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 319

atgtgtgtct taaaagtggc aaatc

25

<210> SEQ ID NO 320

<211> LENGTH: 22

<212> TYPE: DNA

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<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 320

ggaggatgga ctattattgt ag

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<210> SEQ ID NO 321

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 321

gatggcgccg ataggagaga aag

23

<210> SEQ ID NO 322

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 322

ctaaaaagga atattagtat agtg

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<210> SEQ ID NO 323

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 323

gatgaagaga acacatttgg caagtttag

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<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 324

gaggttagcct agtcgaagct ccaaataaag

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<210> SEQ ID NO 325
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 325

gatggctgat aggatcaaag gtccatggag

30

<210> SEQ ID NO 326
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 326

ctcgattctc ccaactccaa tttgactcat

30

<210> SEQ ID NO 327
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 327

atgttccctt ctttcattac tcac

24

<210> SEQ ID NO 328
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 328

attagggttt ttagtaaca cattg

25

<210> SEQ ID NO 329
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 329

atggaaggaa ttcaagcatcc

20

<210> SEQ ID NO 330
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 330

ggcttcatt ttcttgctgg

20

<210> SEQ ID NO 331
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

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<400> SEQUENCE: 331

gatggctggg cgatcatggc tgatc

25

<210> SEQ ID NO 332

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 332

cagcagcgta gcagtgtgtt gcc

23

<210> SEQ ID NO 333

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 333

gatggcggtt gtgggtgaag aagg

24

<210> SEQ ID NO 334

<211> LENGTH: 22

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 334

gaagtcccac aagtcccccc tc

22

<210> SEQ ID NO 335

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 335

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<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 336

tatccgatta tcagaataag aacattc

27

<210> SEQ ID NO 337

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 337

gatgggtctc caagagcttg acccgtagc

30

<210> SEQ ID NO 338

<211> LENGTH: 30

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 338

aataaaacccg aacccactag attgttgacc

30

<210> SEQ ID NO 339
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 339

gatgctgcag tctgcagcac cagag

25

<210> SEQ ID NO 340
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 340

tgaactcacc agtgtcctcc atatac

26

<210> SEQ ID NO 341
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 341

gatggtgaaa gatctggttg gg

22

<210> SEQ ID NO 342
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 342

tctctcgcgta tc当地ttca tcgc

24

<210> SEQ ID NO 343
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 343

atgaagtctt tttgtgataa tgatg

25

<210> SEQ ID NO 344
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 344

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agaatcagcc caagcagcga aaaccgg

27

<210> SEQ ID NO 345
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 345

gatgggtatc caagaaaactg acccgtaac

30

<210> SEQ ID NO 346
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 346

cataaaaccca aacccaccaa cttgccccga

30

<210> SEQ ID NO 347
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 347

gatggtttac ggtaagagat cgag

24

<210> SEQ ID NO 348
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 348

ccaatatatg ttaactattt gtg

23

<210> SEQ ID NO 349
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 349

gatggagaag aggagctcta taaaaaacag

30

<210> SEQ ID NO 350
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 350

tagaaaacaaa caaaaacttat tttcccgata

30

<210> SEQ ID NO 351
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 351
gatggattac gaggcatcaa gaatc 25

<210> SEQ ID NO 352
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 352
gaaattccaa acgcaatcca attc 24

<210> SEQ ID NO 353
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 353
gatggctgat aataaggtca atctttcgat 30

<210> SEQ ID NO 354
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 354
tacagataaa tgaagaagtg ggtctaaaga 30

<210> SEQ ID NO 355
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 355
gatgtacgga cagtgcata tagaatccg 29

<210> SEQ ID NO 356
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 356
tgaaaccaat aactcatcaa cacgtgt 27

<210> SEQ ID NO 357
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 357
ggatggagg gttcgccaa agggctgcga aaagg 35

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<210> SEQ ID NO 358
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 358

atcaaatttc acagtctctc catcgaaaag actcc

35

<210> SEQ ID NO 359
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 359

gatgggtcat cactcatgct gcaaccagca

30

<210> SEQ ID NO 360
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 360

aaacgaagaa gggaaagaag aagataaggc

30

<210> SEQ ID NO 361
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 361

gatggagagc accgattctt ccgggtggtcc

30

<210> SEQ ID NO 362
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 362

agaagagtagc caatttaaac cgggtaattg

30

<210> SEQ ID NO 363
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 363

atggcgacaa ttcagaagct tg

22

<210> SEQ ID NO 364
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

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<400> SEQUENCE: 364	
gtgggttcgat gaccgtgctg	20
<210> SEQ ID NO 365	
<211> LENGTH: 24	
<212> TYPE: DNA	
<213> ORGANISM: Artificial Sequence	
<220> FEATURE:	
<223> OTHER INFORMATION: Synthetic oligonucleotide	
<400> SEQUENCE: 365	
atgtattcat ctccaaagt tc ttgg	24
<210> SEQ ID NO 366	
<211> LENGTH: 24	
<212> TYPE: DNA	
<213> ORGANISM: Artificial Sequence	
<220> FEATURE:	
<223> OTHER INFORMATION: Synthetic oligonucleotide	
<400> SEQUENCE: 366	
acatgagctc ataagaagtt gttc	24
<210> SEQ ID NO 367	
<211> LENGTH: 30	
<212> TYPE: DNA	
<213> ORGANISM: Artificial Sequence	
<220> FEATURE:	
<223> OTHER INFORMATION: Synthetic oligonucleotide	
<400> SEQUENCE: 367	
gatgaattca tttcccacg tccctccggg	30
<210> SEQ ID NO 368	
<211> LENGTH: 30	
<212> TYPE: DNA	
<213> ORGANISM: Artificial Sequence	
<220> FEATURE:	
<223> OTHER INFORMATION: Synthetic oligonucleotide	
<400> SEQUENCE: 368	
cttccataga tcaatctgac aactcgaaga	30
<210> SEQ ID NO 369	
<211> LENGTH: 30	
<212> TYPE: DNA	
<213> ORGANISM: Artificial Sequence	
<220> FEATURE:	
<223> OTHER INFORMATION: Synthetic oligonucleotide	
<400> SEQUENCE: 369	
gatgaacata tcagtaaacg gacagtacaa	30
<210> SEQ ID NO 370	
<211> LENGTH: 30	
<212> TYPE: DNA	
<213> ORGANISM: Artificial Sequence	
<220> FEATURE:	
<223> OTHER INFORMATION: Synthetic oligonucleotide	
<400> SEQUENCE: 370	
tccactaccg ttcaacaagt ggcatgtcgt	30
<210> SEQ ID NO 371	

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<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 371

atggcgaatt caggaaatta tgg

23

<210> SEQ ID NO 372
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 372

aaaaccagaa ttaggaggtg aag

23

<210> SEQ ID NO 373
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 373

atgtgtggag gagctataat ctc

23

<210> SEQ ID NO 374
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 374

aaaagtctcct tccagcatga aattg

25

<210> SEQ ID NO 375
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 375

atggagttca atggtaattt gaatg

25

<210> SEQ ID NO 376
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 376

ttggtagaaag aatgtggagg g

21

<210> SEQ ID NO 377
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 377

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gatgggaagg ggttagggttc aattgaagag 30

<210> SEQ ID NO 378
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 378

tgcggcgaag cagccaagg tgcagttgta 30

<210> SEQ ID NO 379
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 379

gatgggtcgc gaatctgtgg ctgttg 26

<210> SEQ ID NO 380
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 380

ttgtccatta gcattgttct tcttg 25

<210> SEQ ID NO 381
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 381

atggcaacta aacaagaagc tttag 25

<210> SEQ ID NO 382
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 382

agtgacggag ataacggaaa ag 22

<210> SEQ ID NO 383
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 383

atgggtgtcta tgctgactaa tg 22

<210> SEQ ID NO 384
<211> LENGTH: 24
<212> TYPE: DNA

299**300**

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 384

acccaaaagag gagtaattgt attg

24

<210> SEQ ID NO 385
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 385

ggggatggcc aagatggct tgaaac

26

<210> SEQ ID NO 386
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 386

tcaggcctgt tccgatggag gaggc

25

<210> SEQ ID NO 387
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 387

atggaagaat accagcatga caac

24

<210> SEQ ID NO 388
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 388

tcatggaccg agacgataag gtcc

24

<210> SEQ ID NO 389
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 389

gggatggcgt tcgcaggaac aacctcagaaa tg

32

<210> SEQ ID NO 390
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide
<400> SEQUENCE: 390

tttaaggcagcg acgactttgt cc

22

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<210> SEQ_ID NO 391
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide

<400> SEQUENCE: 391

Gly Leu Asp Leu Asp Leu Glu Leu Arg Leu Gly Phe Ala
1 5 10

<210> SEQ_ID NO 392
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(10)
<223> OTHER INFORMATION: Xaa is any amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Xaa is Asn or Glu
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(21)
<223> OTHER INFORMATION: Xaa is any amino acid

<400> SEQUENCE: 392

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Asp Leu Xaa Leu Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa
20

<210> SEQ_ID NO 393
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(10)
<223> OTHER INFORMATION: Xaa is any amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: Xaa is Phe or Ile
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(21)
<223> OTHER INFORMATION: Xaa is any amino acid

<400> SEQUENCE: 393

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Asp Leu Asn Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa
20

<210> SEQ_ID NO 394
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Xaa is Glu, Gln or Asp
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(19)
<223> OTHER INFORMATION: Xaa is any amino acid

<400> SEQUENCE: 394

Leu Asp Leu Asp Leu Xaa Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa
1           5           10          15

Xaa Xaa Xaa

<210> SEQ ID NO 395
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa is Asp, Asn, Glu, Gln, Thr or Ser
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: Xaa is Asp, Gln, Asn, Arg, Glu, Thr, Ser or His
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Xaa is Arg, Gln, Asn, Thr, Ser, His, Lys or Asp

<400> SEQUENCE: 395

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Xaa Leu Xaa Leu Xaa Leu
1           5

<210> SEQ ID NO 396
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa is Asp, Asn, Glu, Gln, Thr or Ser
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: Xaa is Asp, Gln, Asn, Arg, Glu, Thr, Ser or His
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Xaa is Gln, Asn, Thr, Ser, His, Lys or Asp

<400> SEQUENCE: 396

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Xaa Leu Xaa Leu Xaa Leu
1           5

<210> SEQ ID NO 397
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa is Asp, Asn, Glu, Gln, Thr or Ser
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: Xaa is Asn, Arg, Thr, Ser or His

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<400> SEQUENCE: 397

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Xaa Leu Xaa Leu Arg Leu
1           5

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<210> SEQ ID NO 398
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa is Asn, Glu, Gln, Thr or Ser
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: Xaa is Asp, Gln, Asn, Arg, Glu, Thr, Ser or His

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<400> SEQUENCE: 398

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Xaa Leu Xaa Leu Arg Leu
1           5

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25

The invention claimed is:

1. A method for reducing protein productivity in seeds, comprising expressing, in a plant, a chimeric protein obtained by fusing a transcription factor and a functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor,

wherein said transcription factor is a protein comprising the amino acid sequence of SEQ ID NO: 76, or a protein having transactivation activity and comprising the amino acid sequence of SEQ ID NO: 76 but in which 1-10 amino acids have been deleted, substituted, added, or inserted,

and wherein the functional peptide has an amino acid sequence expressed by any one of the following formulae (1) to (8):

(1) X1-Leu-Asp-Leu-X2-Leu-X3 (SEQ ID NO: 392 with deletion of 0-10 residues from the N-terminus) (where X1 denotes a set of 0 to 10 amino acid residues, X2 denotes Asn or Glu, and X3 denotes a set of at least 6 amino acid residues);

(2) Y1-Phe-Asp-Leu-Asn-Y2-Y3 (SEQ ID NO: 393 with deletion of 0-10 residues from the N-terminus (where Y1 denotes a set of 0 to 10 amino acid residues, Y2 denotes Phe or Ile, and Y3 denotes a set of at least 6 amino acid residues);

30 (3) Z1-Asp-Leu-Z2-Leu-Arg-Leu-Z3 (SEQ ID NO: 394 with deletion of 0-10 residues from the C-terminus and deletion of 0-2 residues from the N-terminus) (where Z1 denotes Leu, Asp-Leu, or Leu-Asp-Leu, Z2 denotes Glu, Gln, or Asp, and Z3 denotes a set of 0 to 10 amino acid residues);

35 (4) Asp-Leu-Z4-Leu-Arg-Leu (where Z4 denotes Glu, Gln, or Asp) (residues 4-9 of SEQ ID NO.: 394);

(5) α 1-Leu- β 1-Leu- γ 1-Leu (SEQ ID NO: 395);

(6) α 1-Leu- β 1-Leu- γ 2-Leu (SEQ ID NO: 396);

(7) α 1-Leu- β 2-Leu-Arg-Leu (SEQ ID NO: 397); and

(8) α 2-Leu- β 1-Leu-Arg-Leu (SEQ ID NO: 398)

(where α 1 denotes Asp, Asn, Glu, Gln, Thr, or Ser; α 2 denotes Asn, Glu, Gln, Thr, or Ser; β 1 denotes Asp, Gln, Asn, Arg, Glu, Thr, Ser, or His; β 2 denotes Asn, Arg, Thr, Ser, or His; γ 1 denotes Arg, Gln, Asn, Thr, Ser, His, Lys, or Asp; and γ 2 denotes Gln, Asn, Thr, Ser, His, Lys, or Asp, in formulae (5) to (8)).

40 2. The method according to claim 1, wherein transactivation activity of the transcription factor is repressed.

45 3. The method according to claim 1, wherein the chimeric protein has transcriptional repressor activity.

4. A plant produced by the method of claim 1, wherein said plant exhibits reduced protein productivity in seeds.

* * * * *